

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 14, 2004, 00:01:02 ; Search time 17 seconds  
(without alignments)  
3568.337 Million cell updates/sec

Title: US-10-026-188-8

Perfect score: 6093

Sequence: 1 MDVQPRPGSGDAEDRRE.....HRGGLDGWEQPGAGPPSDT 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2039	33.5	1503	1	TRL2_HUMAN
2	1074	17.6	2032	1	TRFG_CABEL
3	662	10.9	1017	1	TRP3_HUMAN
4	325	5.3	1275	1	TRP3_MOUSE
5	294	4.8	1418	1	CE1L_CABEL
6	266.5	4.4	1124	1	TRFL_DROME
7	264.5	4.3	1172	1	TRP2_MOUSE
8	247	4.1	974	1	TRP5_HUMAN
9	247	4.1	974	1	TRP5_RABIT
10	247	4.1	975	1	TRP5_MOUSE
11	244	4.0	885	1	TRP2_RAT
12	240	3.9	1027	1	TRPL_CABEL
13	226	3.7	981	1	TRP4_BOVIN
14	223.5	3.7	977	1	TRP4_HUMAN
15	220	3.6	974	1	TRP4_MOUSE
16	220	3.6	977	1	TRP4_RAT
17	204.5	3.4	836	1	TRP3_MOUSE
18	201	3.3	931	1	TRP6_HUMAN
19	200	3.3	862	1	TRP7_HUMAN
20	194	3.2	862	1	TRP7_MOUSE
21	193.5	3.2	736	1	TRP3_RAT
22	192.5	3.2	848	1	TRP3_HUMAN
23	190	3.1	930	1	TRP6_MOUSE
24	184.5	3.0	759	1	TRP1_RABIT
25	177	2.9	793	1	TRP1_BOVIN
26	176.5	2.9	759	1	TRP1_RAT
27	176.5	2.9	793	1	TRP1_HUMAN
28	176.5	2.9	809	1	TRP1_MOUSE
29	164.5	2.7	3678	1	DMD_MOUSE
30	159	2.6	432	1	TRP2_BOVIN
31	155	2.5	968	1	PKD2_HUMAN
32	152.5	2.5	966	1	PKD2_MOUSE
33	149	2.4	3680	1	DMD_CANFA

RESULT 1

TRL2\_HUMAN

ID TRL2\_HUMAN STANDARD; PRT; 1503 AA.

AC O94759; O96KNE;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Long transient receptor potential channel 2 (Ltrpc2) (Transient receptor potential channel 7) (TrpC7).

DE TRPM2 OR LTRPC2 OR TRPC7 OR KNP3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;

RX MEDLINE=99026133; PubMed=9806937;

RA Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Asakawa S., Ito F., Shimizu N.;

RT "Molecular cloning of a novel putative Ca2+ channel protein (TRPC7) highly expressed in brain.";

RL Genomics 54:124-131(1998).

[2]

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=22075135; PubMed=11960981;

RA Wehage E., Einfeld J., Heiner I., Jungling E., Zitt C., Luckhoff A.;

RT "Activation of the cation channel long transient receptor potential channel 2 (Ltrpc2) by hydrogen peroxide: A splice variant reveals a mode of activation independent of ADP-ribose.";

RL J. Biol. Chem. 277:23150-23156(2002).

[3]

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20289799; PubMed=10830953;

RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.-S., Toyoda A., Ishii K., Tokoki Y., Choi D.-K., Groner Y., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordliek G., Hornischer K., Brandt P., Scharfe J., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H., Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Vaspo M.-L.;

RT "The DNA sequence of human chromosome 21.";

RL Nature 405:311-319(2000).

CC -!- FUNCTION: May be a calcium channel.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=1;

CC IsoId=O94759-1; Sequence=Displayed;

CC Name=2;

## ALIGNMENTS

34 138 2.3 830 1 VPP3\_HUMAN Q13488 h vacuolar

35 134 2.2 5596 1 MDN1\_HUMAN Q9nu22 homo sapien

36 130.5 2.1 2390 1 SPCP\_HUMAN O15020 homo sapien

37 129.5 2.1 1261 1 APAF\_BRARE Q919h8 brachydanio

38 129.5 2.1 3685 1 DMD\_HUMAN F11532 homo sapien

39 126.5 2.1 2388 1 SPCP\_RAT Q9qwn8 rattus norv

40 126 2.1 5065 1 EPPL\_HUMAN P98107 homo sapien

41 124.5 2.0 1835 1 CCAI\_RAT Q920y8 rattus norv

42 123.5 2.0 2223 1 CCAI\_HUMAN Q9p0x4 homo sapien

43 123 2.0 1060 1 AZ11\_MOUSE Q62036 mus musculu

44 123 2.0 2019 1 C1N5\_RAT P15389 rattus norv

45 121 2.0 805 1 P2LI\_HUMAN Q9p019 homo sapien

```

CC isoid=094759-2; Sequence=VSP_006574, VSP_006575;
CC -!- TISSUE SPECIFICITY: Highly expressed in brain.
CC -!- SIMILARITY: Belongs to the transient receptor family. LTrpC
CC subfamily.
CC -----
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QY 321 EGSELDTVILKALVKACKSHSQBPQDYLDELKLA VAWDRVDIAKSEIFNGDVWKS CD 379
Db 424 DGQODVDVAIIQALLKASRSQDHGHEHNDHQLKLA VAWNRVDIARSEIFMDEWQKPSD 483
QY 380 LEEVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYSVRSKSLIFLLQKQEEA 439
Db 484 LHPMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLPSCLFHSKLOK----- 538
QY 440 RLTLAAGTQOAREPPAGP--PAPSLHEVSVLXDFLQDACRGFYQDGRPCDRR----- 492
Db 539 -----VIVDEPAPACAPAPRLQMHVAVQVLELLGDFTPQPLYPPRHNDRLULLPV 592
QY 493 -----AEKGPAPKPTGCKWLLDINOKSENPRDLFLWAVLQNRHEMATYFWAMGQ 542
Db 593 PHVKLVQGVSLRSLYKRSSGHVTF-----TMDPIRDLIIWAIWVNRRELAGIIWAQSQ 646
QY 543 EGVAAALAAACKILKEMSHLETEAAR---ATRAKYERLALDLFSECYSSEARAFALL 599
Db 647 DCIAAALACSKILKELSEBEDTDSSEMLALAB-EYEHRAIGVFTCYRKDERAQA KLL 705
QY 600 VRRNRCKSTTCLHLATEADAKAFADHGVQAFLTRJWVGDMAGTPTILRLGLAFLCPAL 659
Db 706 TRVSEANGKTTCLQALEAKDMKFVSGGQAFITKVWVGQSLVDNGLWRVTLQWLAPPL 765
QY 660 VYTNLIITFSEEAFLRTGLEDLQDLSDLTEKSPLYGLQSRVEELVEAPRAQGDGRPAVF 719
Db 766 LLTGLISFREKR-----LQD-----VGTFAA----- 786
QY 720 LLTRWRKFWGAPVTYVFLGNVVMYFAFLFTYVLLVDPRPPQSPGSEVTLYFWVFTLV 779
Db 787 ---RARAFFTAPVVVFNHLSYFAFLCLFAYVLMVDFQPV---PSWCECAIYLWLFSLV 840
QY 780 LEEIROGFFTDETHLVKKTFLYVGDNNKDMVAIEFLFVGTVCRLMPSAFAEAGRTVLA 839
Db 841 CEENRQLFYDDECGLMKKAALYFDFWKLVDGAILLFVAGLTCRLIPATLYGRVLS 900
QY 840 MDMVFTLRILHIFAIHKQLGPKIIVVERMMKDVFFLFFLSVLMVAVGVTQALLHPHD 899
Db 901 LDFILCLRLMHIFTISKTLGPKIIVKRWKMDVEFFELFLAVVWSFGVAKQAILIHN 960
QY 900 GLEWIFRRVLYRPLYQIFQIP--LDEIDEARNVCS---THPLLEDSPSCPS----- 948
Db 961 RVDMLFRGAVYHSYLTIFQIGYIDGVANPNPHCSPNGTDPY---KPKCPESDATQQ 1016
QY 949 --LYANWLIVILLFTLLVTNVLMLNLIAMFSYTFQVGNADMFWKFORNYLIVEXHE 1006
Db 1017 RPAPPEWLVLLCLYLLFTNILLNLIAMFNVTFOQVQEBHTQIWKFORHDLIEVHG 1076
QY 1007 RPALAPPFILLSHLSLTLRRVFKBAEHKREHLERDLPDLDQKVVTWETVOKENFLSKM 1066
Db 1077 RPAAPPFPILLSHLQFLFKRVLTKPAKRHKQKLNKLEKNEEAALLSWEIYKENVLQNR 1136
QY 1067 EKRRDSEGEVLRKTAHRVDVFIAYL-----GGLREOEKRIKLESQINYSVLVSS 1118
Db 1137 QFOQKQPEQKIEDISNKDAMVDLLDLDPLKRGSM---EQLASLEEQVAQTARALHW 1193
QY 1119 VADVLAQGGPRSSQHCQEGSQLVAAD---HRGLDGEWQPG 1157
Db 1194 IVRTLASGSGSEADVTLASQKAAEEDPAEPGGRKKTEEPG 1235

```

## RESULT 2

```

TRPG CABEL
ID TRPG CABEL STANDARD; PRT; 2032 AA.
AC Q93971; P91909;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Transient receptor potential channel (Abnormal gonad development
DE protein 2).
GN GON-2 OR T01H8-5/T01H8-3/T01H8-4.
OS Caenorhabditis elegans.

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Db 1244 RSYNNRSDMSKTSVIFGSDPNLSKLQSGNITSTDRPNMBOQFGTRKIMORRRFYEFY 1303  
 Qy 729 GAPVTVLGNVVMFAFLFTYVLLYDRPPPOGSGPEVTLFWVFTLLEBIOGFF 788  
 Db 1304 SAPISTFWSTISFILITFTYLLV--KTPPR-PTVIEVILLAYVAAFGLEQVKLIIM 1360  
 Qy 789 TDETHLVKPKFTLVGNWNKCDMAVIFLVIGVTCRMLPSAFBAGRTVLAMDPMVFTLR 848  
 Db 1361 SDAXP-FYEKIRTVCSFNCVTLIAIFYIVGPFMRFCGVS-AYGRVILACDSVLMTMK 1418  
 Qy 849 LIHFAHKLQKGLPKLIIVERMKDVFFLFLFLSVLWVAYVTTQALLPHDGRLEWIF-R 907  
 Db 1419 LLDYMSVHPKLGPTVTMAGKIQMNSYIIVLVTLISFGLAROSITYP-DETHWILVR 1477  
 Qy 908 RVLRYRPLQFGQPLDEIDARVNCSTH-----PULLEDSP---SCPSLYANWL 954  
 Db 1478 NIFKLPFMLYGEVYADEID---TCGDEAWDQHLNGPVLNGTGLSCVPGY--WI 1531  
 Qy 955 VILLVTVLLVTVNLLNMLLAMSFTYQVVGQADMFVKQRYNLIIVEYHERPALAPPF 1014  
 Db 1532 PPLMTFTLLTANILLMSLIAIENHIFDATDMSQIWLQRYKQVMEYESTPFLPPL 1591  
 Qy 1015 ILLSHLSLTIR---RVFKKAEKREHLERDLDPDLD---QKVVTVETVQKENFL-SK 1065  
 Db 1592 TPLVHGVLIIQFVTRTSCSKSQERNPMFDFSLKFLDNDQIEKLHDFEEDCMEDLARQK 1651  
 Qy 1066 MEKRRRSEGBVLKRTAHR-----VDFAKYLG--LREQEKRIKCLSESQINYSVL 1115  
 Db 1652 LNEKNTSNEQRIILRADIRTDQILNRLIDLQAKSGRVDINDVESRLASVEKAQN--EI 1708  
 Qy 1116 VSSVADVLIAQGGPRSSQHC 1135  
 Db 1709 LECVRALLNQNNAPTIGRC 1728

## RESULT 3

TRL3 HUMAN  
 ID - TRL3 HUMAN STANDARD; PRT; 1017 AA.  
 AC Q9HCF6;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Long transient receptor potential channel 3 (LTrpC3) (Fragment).  
 GN TRPM3 OR LTRPC3 OR KIAA1616.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE=20450683; PubMed=10997877;  
 RX Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes.  
 RT XLIII. The complete sequences of 100 new cDNA clones from brain which  
 RT code for large proteins in vitro.";  
 RL DNA Res. 7:273-281(2000).  
 CC -!- FUNCTION: May be a calcium channel.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -!- SIMILARITY: Belongs to the transient receptor family. LTrpC  
 CC subfamily.

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DR EMBL; AB046836; BAB13442.1; -  
 DR Genew; HGNC:17992; TRPM3.  
 DR InterPro; IPR002111; Cat\_channel\_Trlp.

DR InterPro; IPR005821; Ion\_trans.  
 DR Pfam; PF00520; ion\_trans; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel.  
 FT NON\_TER 1 1  
 FT TRANSMEM 80 100 POTENTIAL.  
 FT TRANSMEM 183 203 POTENTIAL.  
 FT TRANSMEM 250 270 POTENTIAL.  
 FT TRANSMEM 314 334 POTENTIAL.  
 FT TRANSMEM 402 422 POTENTIAL.  
 FT TRANSMEM 453 473 POTENTIAL.  
 SQ SEQUENCE 1017 AA; 116681 MW; B088354F100A972C CRC64;

Query Match 10.9%; Score 662; DB 1; Length 1017;  
 Best Local Similarity 28.0%; Pred. No. 1.5e-36;  
 Matches 171; Conservative 135; Mismatches 247; Indels 58; Gaps 14;

Qy 576 YERLALDLPECYSNSARAFALIVRRNRCSKTTCLHLATEADAKAFFAHGQVQALTR 635  
 Db 10 FGQAVELLDQSYKQDQLAKWLLTYELKNWSNATCQLQVAAKHDFIAHTCSQMLTD 69  
 Qy 636 IWWG--DMAAGTPTILRLIGAFPCALV---YTNLITFSEEAFLRTGLE--LQDLDSLD 688  
 Db 70 MWMGRLMRKNKSGLVILGPSILSLFKN---KDDMPYMSQAEIHLQKEAEEP 125  
 Qy 689 EKSPYGLQSRVELVAPRAQDRG-----PRAVLLTRWRKFWGAPVTVPLG 737  
 Db 126 EKPTKEKEEEDMELTAMLGRNNGSSSRKDEEVSQSKRLIPLGRKIYEFYNAPVFWF 185  
 Qy 738 NVVMYFAFLFTVTVLAVDRPPPGQSGPEVTLFWVFTLLEBIOGFFTDTHLVK 797  
 Db 186 YTLAYIGYLMFLNFIYLVKME---RWPSTQEWIVISYITFLGIEKRE--ILMSFGKLLQ 241  
 Qy 798 KFTLYVGDNNKCDMAVIFLVIGVTCRMLPSAFE--GRVVLAMDPMVFTLRLIHF 856  
 Db 242 KVKVWLQYWNVTDLIALLLFSVGMILRLQDQPPSGRVIYCVNIIYVIRLLDIFGN 301  
 Qy 857 KQGPKLIIVERMKDVFFLFLSVLWVAYVTTQALLPHDGRLEWIFRVLRYPLQ 916  
 Db 302 KYLGFYVMIGKIMIDMYFIIMLVLMFGVARQAILFNEEPSKWLAKNIIFYMPYMW 361  
 Qy 917 IFGOIPLDEIDARVNCSTHPLLEDSS---PSCPILYANWLVLVTLVTVNLLM 971  
 Db 362 IYGSVFADQIDPPGQNETR---EDGKIQLPCKT--GAWIVPAIMACVLLVANILLV 415  
 Qy 972 NLLIAMSFTYQVVGQADMFVKQRYNLIIVEYHERPALAPPFILLSHLSLTIRVFKKE 1031  
 Db 416 NLLIAVNNITFEVKISINQWKQRYQLIMTPHERPVLPPPLIFSHMTMIFQHLCCRW 475  
 Qy 1032 AEKREHLERD-----LPDPLDQVTVETVQKENFLSKMEKRRRDSGEVLRKTAHRV 1085  
 Db 476 RKHSDPDDERDYGLKLFITDDLKKVHDFEEQCEIEYFREKDDRFNSNDRIRVTSERV 535  
 Qy 1086 DFIAYLGLGREQEKRIK---LESQINYSVLVSSVADVLIAQGG-----PRS 1131  
 Db 536 ENMSRLVEEVNREHSMKASLQTVDIRLAQLEDLIGRWATALERLTGLERAESNKIRST 595  
 Qy 1132 SQHCGEQSOLV 1142  
 Db 596 SSDCTDAAYIV 606

## RESULT 4

TRP\_DROME  
 ID - TRP\_DROME STANDARD; PRT; 1275 AA.  
 AC P19334;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Transient receptor potential protein.  
 GN TRP.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_taxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Oregon-R;  
RX MEDLINE=90180449; PubMed=2516726;  
RA Montell C., Rubin G.M.;  
RT "Molecular characterization of the Drosophila trp locus: a putative  
RT integral membrane protein required for phototransduction.";  
RL Neuron 2:1313-1323(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90148782; PubMed=2482778;  
RA Wong F., Schaefer E.L., Roop B.C., Lamendola J.N., Johnson-Seaton D.,  
RA Shao D.;  
RT "Proper function of the Drosophila trp gene product during pupal  
RT development is important for normal visual transduction in the  
RT adult.";  
RL Neuron 3:81-94(1989).  
RN [3]  
RP SEQUENCE OF 1126-1275 FROM N.A.  
RX MEDLINE=88042982; PubMed=3118483;  
RA Wong F., Yuh Z.T., Schaefer E.L., Roop B.C., Ally A.H.;  
RT "Overlapping transcription units in the transient receptor potential  
RT locus of Drosophila melanogaster.";  
RL Somat. Cell Mol. Genet. 13:661-669(1987).  
CC -!- FUNCTION: REQUIRED FOR PHOTOTRANSDUCTION. SUGGESTED TO MEDIATE  
CC -!- CALCIUM ENTRY. SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT  
CC CHANNEL.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC  
CC MEMBRANES OF THE PHOTORECEPTOR CELLS.  
CC -!- SIMILARITY: Belongs to the transient receptor family. STRpC  
CC subfamily.  
CC -!- SIMILARITY: Contains 2 ANK repeats.  
CC  
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CC  
DR EMBL; M34394; AAA28976.1; -;  
DR EMBL; M21306; AAA56928.1; -;  
DR EMBL; M18634; AAA28977.1; -;  
DR FlyBase; FBgn0003861; trp.  
DR GO; GO:0016028; C:ribosome; IDA.  
DR GO; GO:0015279; F:store-operated calcium channel activity; NAS.  
DR GO; GO:0008377; P:light-induced release of calcium, from inte. .; IDA.  
DR GO; GO:0009416; P:response to light; IMP.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR002111; Cat channel\_TrpL.  
DR InterPro; IPR005821; Ion trans.  
DR InterPro; IPR002153; Trans receptor.  
DR InterPro; IPR004729; Trp\_CaChannel.  
DR Pfam; PF00023; ank; 2.  
DR Pfam; PF00520; ion trans; 1.  
DR PRINTS; PR01097; TRNSRECEPTRP.  
DR SMART; SM00248; ANK; 2.  
DR TIGRFAMs; TIGR00870; trp; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;  
KW Vision; ANK repeat; Repeat.  
FT DOMAIN 1 366 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 367 387 POTENTIAL.  
FT DOMAIN 388 390 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 391 411 POTENTIAL.  
FT DOMAIN 412 418 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 419 439 POTENTIAL.  
FT DOMAIN 440 450 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM	451	471	POTENTIAL.
FT DOMAIN	472	507	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	508	528	POTENTIAL.
FT DOMAIN	529	541	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	542	562	POTENTIAL.
FT DOMAIN	563	638	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	639	659	POTENTIAL.
FT DOMAIN	660	1275	EXTRACELLULAR (POTENTIAL).
FT REPEAT	69	98	ANK 1.
FT REPEAT	143	172	ANK 2.
FT CONFLICT	285	288	GQRQ -> ASSE (IN REF. 2).
FT CONFLICT	326	329	RRKQ -> PQE (IN REF. 2).
FT CONFLICT	365	374	KPFVKFTHS -> NPLSSSRTP (IN REF. 2).
FT CONFLICT	785	785	S -> N (IN REF. 2).
SQ SEQUENCE	1275 AA;	142589 MW;	91CFCD9896989B1 CRC64;

Query Match 5.3%; Score 325; DB 1; Length 1275;  
Best Local Similarity 20.0%; Pred. No. 1.1e-13;  
Matches 184; Conservative 133; Mismatches 275; Indels 328; Gaps 39;

QY	274	VPKVAEK-QFKEKPSKHSFMSDIVRWTKLQNTISH-----OHLTVYDPEQEGS	323
Db	48	VKKILEYQGTDKP---NINCTDPNRSALISAENENFDLMVILHNIEVGDALLHAI	104
QY	324	BEIDTVILKALVKACKSHSQPDYLDLKLAVADRVDIKAKSEIPNGDVEWKSCDLEEV	383
Db	105	SEEVYEAVEELLQWEETNHKEGQPY-----SWEAVDRSKS-TFTVDI-----TP	147
QY	384	MYDALVSNKPEFVRLFVNGA-----DVADFLTYGELQ-ELYSYSR	424
Db	148	LILAAHRNYYEILKILLDRGATLPMHVDKCGCECVTSQTTDSLHSHQSRINAYRALSA	207
QY	425	KSLLDLLQKQEEARLTLAGLTQCAREPPAGPAFSLHVSRLK--DFLQDACRGFY	482
Db	208	SSLI-----ALSSRD-----PVLTVFQLSWELKRLQAMESFEABY	243
QY	483	QDGRPGDRRAEKGPAKPTQKWLIDLNLQKSENPRDLFLWAVLQNRHEMATYFWAMQ	542
Db	244	TEMR---QWQDFGTS-----LLDHARTS-----MELEVMLNHNHPSHDIWCLQ	286
QY	543	EGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLVR	602
Db	287	-----RQTLER-----	292
QY	603	NRCWSKTTCLHATEADAKAPFAHDGVOAFTRIWGDMAAGTPIRLLLGALCPALVYT	662
Db	293	-----LKLAIRYKOKTFAHNVVQOLAAAIWD---GLPGFR-----	326
QY	663	NLITFSEBAPLRTGLDLDLSDTEKSPLYGLQSRVEELVEAPRAQDGRPAVFLLT	722
Db	327	-----RKQASQQLMDVVKLGCSFPYVSL-----KVILAPDSEG-----	359
QY	723	RWRKFWGAPVTVFLGNVVMYFAFLF-----FTYVL--LYDPRPPQG	763
Db	360	--AKEMRKPFVKFTHSCSYMPFLMLLGAASLRVVQITFELLAFPMWLTMLDWRKHG	417
QY	764	--PSGPEVTLVFWFTLVLEIR-----OGFTDEDTHLVKFTLVYGNWNKCDMVAIFL	817
Db	418	SUPGPIELAIITYIMALIFEELKSLYSDGLFE-----YIMDLNIVDIYSNMF	465
QY	818	FIVGVTCR-----MLPS--AFEAGRTVLAMDWMVF	845
Db	466	VVTWILCRATAWIVHRDLWFRGIDPYFPREHWHFDPMLLSEGAFAG-----WVF	517
QY	846	T-LRLIHIFAIKQGPKIIVVERMKDVFFFLFSLWLVAYGVTTQALL-----	895
Db	518	SYLKLVIHIFSINPHLGLQVSLGRMIIDIKEFFIYTLVLFAGCGNLNOLLWYAELEKN	577
QY	896	---HCHDGRLEW-----IFRRV--LYRP-----YLQIFGOIPLDEIDEARVNCSTHPL	938
Db	578	KCYHLHPDVADFDQOEKACTWRRFSNLFETSQSLFWASGLVDLVSFDLGKIS-----	632
QY	939	LLEDSPSPCPSLYANWLVILLVTLFLLVTLNVLNLLIAMFSYTFQVQGNADMFWKFOR	998

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633 -----FTRFWALLMEGSSVINIIVLLNMLIAMMSNYQIISERADTEWKFARS 681
999 NLIVEYHE-RPALAPPFILLSHLSJTLRRVFKAEHKEHLERDL--PDLDQKVVTWE 1055
682 QLMWSYFEDGGTIPPPFNLCNMKRLKTLGRKSPRTSKSPMRKSMERAQTLHDKVM--- 738
1056 TVQKENFLSKMEKRRDSEG 1075
739 KLLVRYIT-AEQRRRDYG 757

RESULT 5
ID CE11 CAEEL STANDARD; PRT; 1418 AA.
AC P34641;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ced-11 protein.
GN CED-11 OR ZK512.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -----
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CC -----
CC EMBL; Z22177; CAA80145.1; --
CC PIR; S40764; S40764.
CC WormPep; ZK512.3; CE00409.
CC InterPro; IPR002111; Cat Channel TrpL.
SQ SEQUENCE 1418 AA; 159237 MW; 4FC83B9E7ADF7788 CRC64;

Query Match
Best Local Similarity 4.8%; Score 294; DB 1; Length 1418;
Matches 222; Conservative 174; Mismatches 437; Indels 264; Gaps 45;

65 PNLVSVLGEQPPFAMKSWLRDLVRKGLVKAQSTGAWILTSALRVGLRHVGQVRDHS 124
67 PDLIISLISHGNSLSTK--YMSSEVNGLSKFLIGCGTWLISSG-----EVNDPM 113
125 LASTSTKRVVAVGMSLGRVLRHRLLEEAEQEDFVHYPEDGGSQGPLCSLDSNLSHFI 184
114 SRVAGALKNVLPQLEHQAEVLH--ILVNSDD----MTASDTTNSKS---VVDTSINTLL 164
185 LV---EFGPGKGDGLTELRLEKHI-----SE--QRAGYGGTGSi----- 221
165 LICRKEFNDSEYETVASSIAKLRAATAVLAHPHPPALLIGVSEPMSPSTYNSAAILLSP 224

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RESULT 6

TRPL DROME

ID TRPL DROME STANDARD; PRT; 1124 AA.

AC P48994; Q9V5B2;

DT 01-FEB-1996 (Rel. 33, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

QY 222 -----EIPVLCCLVNGDPTLERISRAVEQAAPMLILVGGGIADVLAAALVNQPHLLVPK 276
DB 225 SNDKRPPEV-AIPAGAKESIELLFFVEHIGIPVILLQDS-----CELCAILHSHSHELL-- 277
QY 277 VAEQKFKPEPSKHSFMSMEDIVRWTKLQNIITSHOHLITVYDFQEGSEELDTVLKALVK 336
DB 278 -----ETSNFNDNDKFISW-----LRSQLYPL-----GLADCYTLITKLIV- 312
QY 337 ACKSHSQEPQ--DYLDLKLAVANDRVDIKASEIFNGDVEMKSCDLEB--VMVDALVSNK 392
DB 313 --SSNGDVQLIEFIDSSQSE-----LSSVVVDRCLECYATTGEERQVLLLAALNS 363
QY 393 PEFVRLFVDNGADVADFLTYGRLOELYSVRKSKLLFDLLQKQKQBEARLTLAGLGTQOAR 452
DB 364 PS-VLSMDVAQAQDDELLTILCEITKDDQLHFLSSVLO----- 403
QY 453 EPPAGPPAFSLHEVSRVLKDFLODA-----CRGYQDGRPGDRERRA---EKG 497
DB 404 ---LSPP---IRVTSNMLRMHMHADHFFTTIVLCQCMGYSTIPSEIDPRFANDIQKLV 457
QY 498 AKRPTGQKWLDDLN-----QKSENPRWDLFLWAVLQNRHEMATYFWANGQGVAAAL 549
DB 458 KKLSTFGVDNLFDPNVFONDSSHRDKHSIRLAIWSLLHHPGIVKCLAAFADEPFAESM 517
QY 550 AACKILKEMSHLETE--AEAARATREAKYERLALDLFSECYNSSEARAFALLVRNRNCW 606
DB 518 VLSRIARSLGHESHDFEYKSLNLTSDLSGSAITLFDTVFTSPAKAYQLLQCPMEYF 577
QY 607 SKTTLHLATEADAKAFPHDGVQAFTRIWMGDM-AAGTPIRLKLLGAFICPALV----- 660
DB 578 YGFNMTQLAFHCNAREIIAHECCQWRVHRKLYGNLQAKNFFIPLPKWAKICISAVLIIPV 637
QY 661 -----YTNLITFSE-----EAPLRGL 677
DB 638 KFMVLVPRERTKQDTPVTVALLDVGKFPQKQRAISTYVISRSSEALFALTAPLSTAF 697
QY 678 EDLQDLSD--TEKSPLYGQSREBELVEAPRAQGD---RGPRAVFLLTRWRKFWGAP 731
DB 698 GFNSALNGAESATPQSMVFPPL--NIEIDKDPFGKKNRIRRAHAHTLST---FYSTP 751
QY 732 VTVEFGNVMYFAFLFTTVLLVDPRPPQPGSGPEVTLYFVFTVLVLEEIRQGFDTDE 791
DB 752 IVKYWLSLFRIVPICCLAYSVVL-----PGCGSNLNDTGMWWSF-----FWWIE 797
QY 792 D---THLVKKFTLYVGDNNKNCMDVAIFLFIIVGVTCTRMCLPSAFEAGRT--VLAMDWFVF 845
DB 798 NCFVLTARAKIPLSLMP-WRVFDFVFAFFVFLI---LLLVNKVFPVTFVLEVLGID-SIY 852
QY 846 TLRLEHIF-----AIHKQLGPKIIVVERM-MKDVFFFLFFLSVWLVAYGVT 890
DB 853 SAKVVSFAFFVLYVSYSTLFTVPLSDIFGPMIVRVKMLMLLRDFTNLFMLIALVMSAVA 912
QY 891 TOALLHPHGRLEWIFRVLRYRPLYQIFGQIPDLDEIDARV-----NCSTHPLL 939
DB 913 IQAVFPDRPVTWEVFRKTLISWLSLF-TTDLSNLSESECTCKSFLGAPKRYCSS--VG 969
QY 940 LEDSPSCPSLVANWLVILLVTLVTLNVLNMLLIAMFSYTFQVQGNADMFKFORYN 999
DB 970 QYANPSCPS--QSLPAYLIVIEYFVILKLLLPILFAFFSKTAKNVDDDEADKIWRFLYS 1027
QY 1000 LIVEYHERPALAPPFIL 1016
DB 1028 LAEDFLRLRPPLPPLTI 1044

```

Transient-receptor-potential like protein.

TRPL OR CG18345/CG1694.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Oregon-R;

RA MEDLINE=92232293; PubMed=1314616;

RA Phillips A.M., Bull A.L., Kelly L.E.

RT "Identification of a Drosophila gene encoding a calmodulin-binding

RT protein with homology to the trp phototransduction gene.";

RL Nucleon 8:631-642(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkley;

RA MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananthides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.O., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

CC -1- FUNCTION: BINDS CALMODULIN. SUGGESTED TO MEDIATE CALCIUM ENTRY.

CC -1- SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT CHANNEL.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC

CC -1- MEMBRANES OF THE PHOTORECEPTOR CELLS.

CC -1- SIMILARITY: Belongs to the transient receptor family. StrpC

CC subfamily.

CC -1- SIMILARITY: Contains 2 ANK repeats.

CC

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF054568; AAC00002.1; -;  
 CC EMBL; AC005191; AAC24563.1; -;  
 CC EMBL; AL049563; CAB44737.1; -;  
 CC Genew; HGNC:12337; TRPCS.  
 CC MW; 300334; -;  
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.  
 CC GO; GO:0015279; F: store-operated calcium channel activity; TAS.  
 CC GO; GO:0006816; P: calcium ion transport; TAS.  
 CC GO; GO:0007399; P: neurogenesis; TAS.  
 CC InterPro; IPR002110; Cat channel\_TripL.  
 CC InterPro; IPR002111; Ion trans.  
 CC InterPro; IPR005821; Ion trans.  
 CC InterPro; IPR002153; Trans receptor.  
 CC InterPro; IPR004729; Trp CaChannel.  
 CC InterPro; IPR005461; TRPChannel5.  
 CC Pfam; PF00023; ank; 2.  
 CC Pfam; PF00520; ion trans; 1.  
 CC PRINTS; PR01097; TRNSRECEPTR.  
 CC PRINTS; PR01646; TRPCHANNEL5.  
 CC SMART; SM00248; ANK; 2.  
 CC TIGRFAMs; TIGR00870; ttp; 1.  
 CC PROSITE; PS00088; ANK\_REPEAT; FALSE NEG.  
 CC PROSITE; PS02097; ANK\_REPEAT\_REGION; FALSE NEG.  
 CC Ionic channel; Transmembrane; Ion transport; Calcium channel;  
 KW ANK repeat; Repeat; Glycoprotein.  
 FT DOMAIN 1 330 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 331 351 POTENTIAL.  
 FT DOMAIN 352 398 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 399 419 POTENTIAL.  
 FT DOMAIN 420 437 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 438 458 POTENTIAL.  
 FT DOMAIN 459 470 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 471 491 POTENTIAL.  
 FT DOMAIN 492 512 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 513 533 POTENTIAL.  
 FT DOMAIN 534 603 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 604 624 POTENTIAL.  
 FT DOMAIN 625 973 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 69 98 ANK 1.  
 FT REPEAT 141 170 ANK 2.  
 FT SITE 971 973 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN  
 (BY SIMILARITY).  
 FT CARBOHYD 461 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT SEQUENCE 973 AA; 111411 MW; FBC8CBF17BE42166 CRC64;  
 Query Match 4.1%; Score 247; DB 1; Length 973;  
 Best Local Similarity 21.8%; Pred. No. 1.3e-08;  
 Matches 143; Conservative 93; Mismatches 229; Indels 190; Gaps 27;  
 QY 555 LKMSHLETEAARATREAKYERLALDLFSECSNSEARAFALLVRRN-----RCW 606  
 DB 227 LKLSKVNEFKAYEELSQCKLFAKLLDQARSRELE--IILNHRDDHSEELDPQKY 284  
 QY 607 SKTCTLHLATEADAKAFHAGDGVQAFLTRIWGDMAGTP-----ILRLIG----AFL 655  
 DB 285 HDLAKLVAIKVHQKEFVAQPNQCQLLATLWDYD---GFGWRKRHHVVKLLTCMTIGFL 340  
 QY 656 CPALVYTNLTSEEARPLRTGLDLDLSLDTKSPLYGLQSRVEELVEAPRAQDRGP 715  
 DB 341 FPMLSIAYLIS-----  
 QY 716 RAVFLLTRWRKFWGAPVTVFLGNVVMYFAFLFLF----TYVLLVDFRPPPPQSGPEVIL 771  
 DB 353 RSNLGL-----FIKKPFPIKCHTASVTLFLFMILLASQHVIRTDLHVQGPPTVVEWMI 407  
 QY 772 YFWVFTLVLEIRQ---GFTDEBTHLVKKFTLYVGDWNKCDMVAIFLFIUGVTCRMLP 828

Db 408 LPWVLGFIWGEIEMMDGGFTE-----YIHDWNLMDFAMNSLALATISLIVA 456  
 QY 829 SAFEAG-----RTVLAMDWFVFTLRILHIFAIHKQLGPKIIVVERMKD 872  
 Db 457 YVKNGRPREEWEMWHPITLAEALFAISNLISLISLFTANSGLPLQISLGRMLLD 516  
 QY 873 VFFFLFELSVMLVAYG-----VTQALLHPH-----DGRLEWIFRVLVYRP 913  
 Db 517 ILKFLFIYCLVLLAFANGLNQLFYVYETRAIDENCKGIRCEKQNNAFSTLP-ETLQSL 575  
 QY 914 YLQIFGQIPLDEID-EARVNCSTHPLLEDSPSCPSLYANWLVILLVLTLLVTVNVLN 972  
 Db 576 FWSYFGLNLVYTNVKAR-----HE-----FTEFVGATMGTNYNIVISLVLLN 618  
 QY 973 LLIAAFSYTFOVQGNADMFWKFORYNLIVEY-HERPALAPFP-ILLSHLS-LTLRRVFK 1029  
 Db 619 MLIAMNNSQLIADHADIEWKPARTKLWMSYFDEGGTLPPFNIIPSPKSFYLGWNFN 678  
 QY 1030 KEAEHKREHLERDLPDLPDQKVTVQKNEFLSKMEKRDS-----EGEVLKRTAH 1083  
 Db 679 NTFCKRD-----PDGR-----RRRNLRSEFTERNADSLIQNHQYQEVIRNLVK 722  
 QY 1084 RVDIA-----KYLGLRGE-KRIKLESOINYCSVLVSSVADVLAQGGGPRS 1131  
 Db 723 R--YVAAMIRNSKTHEGLTEENFKELQDISSFRY-----EVLDDLGNRKHPRS 769  
 RESULT 9  
 TRP5\_RABIT  
 ID TRP5\_RABIT STANDARD; PRT; 974 AA.  
 AC 062852;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Short transient receptor potential channel 5 (TrpCs) (Rtrps)  
 DE (Capacitative calcium entry channel 2) (CCE2).  
 GN TRPCS OR TRPS.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RC MEDLINE=98353453; PubMed=9687496;  
 RA Philipp S., Hambrecht J., Braslavski L., Schroth G., Freichel M.,  
 RA Murakami M., Cavalie A., Flockerzi V.;  
 RT "A novel capacitative calcium entry channel expressed in excitable  
 cells.";  
 RL EMBO J. 17:4274-4282 (1998).  
 CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE  
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A  
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR  
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN  
 CC SHOWN TO BE CALCIUM-SELECTIVE. MAY ALSO BE ACTIVATED BY  
 CC INTRACELLULAR CALCIUM STORE DEPLETION.  
 CC -!- SUBUNIT: INTERACTS WITH NHERF (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in brain.  
 CC -!- SIMILARITY: Belongs to the transient receptor family. STpC  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 2 ANK repeats.  
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 CC -----  
 CC EMBL; AJ006203; CAA06911.1; -;

DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR002111; Cat channel\_Trip.  
 DR InterPro; IPR005821; Ion trans.  
 DR InterPro; IPR002153; Trans receptor.  
 DR InterPro; IPR004729; Trp CaChannel.  
 DR InterPro; IPR005461; TRPChannels.  
 DR Pfam; PF00023; ank; 2.  
 DR Pfam; PF00520; ion trans; 1.  
 DR PRINTS; PR01097; TRNSRECEPTP.  
 DR PRINTS; PR01646; TRPCHANNELS.  
 DR SMART; SM00248; ANK; 2.  
 DR TIGRams; TIGR00870; trp; 1.  
 DR PROSITE; PS00088; ANK REPEAT; FALSE NEG.  
 DR PROSITE; PS0297; ANK REP REGION; FALSE NEG.  
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;  
 KW ANK repeat; Repeat; Glycoprotein.  
 FT DOMAIN 1 330 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 331 351 POTENTIAL.  
 FT DOMAIN 352 398 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 399 419 POTENTIAL.  
 FT DOMAIN 420 437 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 438 458 POTENTIAL.  
 FT DOMAIN 459 470 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 471 491 POTENTIAL.  
 FT DOMAIN 492 512 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 513 533 POTENTIAL.  
 FT DOMAIN 534 603 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 604 624 POTENTIAL.  
 FT DOMAIN 625 974 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 69 98 ANK 1.  
 FT REPEAT 141 170 ANK 2.  
 FT DOMAIN 690 693 POLY-ARG.  
 FT SITE 972 974 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN (BY SIMILARITY).  
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. ) (POTENTIAL).  
 SQ SEQUENCE 974 AA; 111536 MW; 942566OP28923316 CRC64;  
 Query Match 4.1%; Score 247; DB 1; Length 974;  
 Best Local Similarity 21.8%; Pred. No. 1.3e-08;  
 Matches 143; Conservative 94; Mismatches 229; Indels 190; Gaps 27;  
 QY 555 LKEMSHLEAEARATRAKRYERLALDFSECYNSSEARAFALLVRN-----RCW 606  
 DB 227 LKELSKVENEFKAEYELSEQQCKLFAKDLDDQARSRELE--IILNHRDDHSELDPPQKY 284  
 QY 607 SKTTCILHLATEADAKAFFAHGQVAFLTRIWMGDMAAGTP-----ILRLLG---AFL 655  
 DB 285 HDLAKLVAIKYHQEFVQPNQCQLLATLWD-----GPPGWRKHVVVKKLLTCTMTIGEL 340  
 QY 656 CPALVYTNLITFSEAPLRATGLDQLDLSLDTESKSPLYGLOSRLVEELVEAPRAQGDGRGP 715  
 DB 341 FPMLSIAYLIS-----YHDDWNLDMFAMNSLYLATISLKIVA 456  
 QY 716 RAVFLLTRWRKENGAPVTVELGNVVMYFAFLFLF-----TYVLLVDRPPPPQSGSDEVTL 771  
 DB 353 RSNLGL-----FIKKPFIFKICHTASYLTLFPLMLLASQHVIRTDLHVQGPPTVVEWMI 407  
 QY 772 YEWVFTLVLEIRQ--GFPTDETHLVKKFTLYGDNWKNKDMVAIFLFIIVGTCRMLP 828  
 DB 408 LPWVLGFIWGLKEMWDGGFTF-----YHDDWNLDMFAMNSLYLATISLKIVA 456  
 QY 829 SAFEAG-----RTVLAMDPMVFTLRLIHFIAHFKQLGPKIIVVERMKMD 872  
 DB 457 YVYNGSRPREEMWHP\*LIAEALFAISNILLSRLISLFTANSGLPLQLSLGRMLD 516  
 QY 873 VFFFLFFLSVWLAVG-----VTQALLHPH-----DGRLEWIFRVLVYRP 913  
 DB 517 ILKFLFIYCLVLLAFANGLNQLFYFYETRAIDEPNNCKGIRCEKQNNAPSTLF-ETLQSL 575  
 QY 914 YLQIFGQPLDID--EARVNCSTHPLLEDSDSCPSLYANWLVIALLVTLFVTLVLMN 972  
 DB 576 FWSVFGLNLYTNVKAR-----HE-----FTEFGATMGFTGYINVISLWLLN 618

QY 973 LLTAMPSYTPQVVOGNADMEWKFORYNLIVEY-HERPALAPPF-ILLSHLS-LTLRRVFK 1029  
 DB 619 MLTAMWNSYQLADHADIWKFKATLWMSYFDEGGTLPPFPNIPSPKSFYLGWNFN 678  
 QY 1030 KEAEHKREHLERDLPDLDQKVVTWETVKENFLSKMEKRRDS-----EGEVLKRTAH 1083  
 DB 679 NTECPKRD-----PDGR-----RRRNLRSFETRHADSLIQNHQYQEVIRNLVK 722  
 QY 1084 RVDFA-----KYLGLRQE-KRIKLESQINYSVLVSSVADVLAAQGGPRSS 1132  
 DB 723 R--YVAAMIRNSKTNEGLTEENFKELQDISFRY-----EVLDLLGNRKQPPRS 770  
 RESULT 10  
 TRPS MOUSE  
 ID -TRPS\_MOUSE STANDARD; PRT; 975 AA.  
 AC Q9OX29; Q61059; Q9QWT1; Q9R0D4;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Short Transient receptor potential channel 5 (TrpC5) (Transient receptor protein 5) (TrpP5) (trp-related protein 5) (Capacitative calcium entry channel 2) (CCE2).  
 DE TRP5 OR TRP5 OR TRP5.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98221157; PubMed=9553080;  
 RA Okada T., Shimizu S., Wakamori M., Maeda A., Kurosaki T., Takada N., Imoto K., Mori Y.;  
 RT "Molecular cloning and functional characterization of a novel receptor-activated TRP Ca2+ channel from mouse brain."; J. Biol. Chem. 273:10279-10287(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Zhu X., Peyton M., Boulay B., Birnbaumer B.;  
 RT "Molecular cloning and functional expression of mouse TRP5."; Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20545496; PubMed=10980202;  
 RA Tang Y., Tang J., Chen Z., Trost C., Flockerzi V., Li M., Ramesh V., Zhu M.X.;  
 RT "Association of mammalian trp4 and phospholipase C isozymes with a PDZ domain-containing protein, NHERF."; J. Biol. Chem. 275:37559-37564(2000).  
 RN [4]  
 RP SEQUENCE OF 1-966 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=98333453; PubMed=9687496;  
 RA Philipp S., Hambrecht J., Braslavski L., Schroth G., Freichel M., Murakami M., Cavalie A., Flockerzi V.;  
 RT "A novel capacitative calcium entry channel expressed in excitable cells."; EMBO J. 17:4274-4282(1998).  
 RN [5]  
 RP SEQUENCE OF 515-637 FROM N.A.  
 RX MEDLINE=96234226; PubMed=8646775;  
 RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E., Birnbaumer L.;  
 RT "trp, a novel mammalian gene family essential for agonist-activated capacitative Ca2+ entry."; Cell 85:661-671(1996).  
 RL Cell 85:661-671(1996).  
 CC !- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY A TYROSINE KINASE OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN SHOWN TO BE CALCIUM-SELECTIVE. MAY ALSO BE ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.





CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- SIMILARITY: Belongs to the transient receptor family. Strpc  
 CC subfamily.  
 CC -1- SIMILARITY: Contains 3 ANK repeats.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AJ276027; CAC81654.1; -  
 CC EMBL; L16685; AAA28167.3; -  
 CC F01; S44872; S44872.  
 CC WormPep; ZC21.2; CE33009.  
 CC InterPro; IPR002110; ANK.  
 CC InterPro; IPR002111; Cat\_channel\_TrpL.  
 CC InterPro; IPR005821; Ion trans.  
 CC InterPro; IPR002153; Trans receptor.  
 CC InterPro; IPR004729; Trp\_CaChannel.  
 CC Pfam; PF00023; ank; 2.  
 CC Pfam; PF00520; ion trans; 1.  
 CC PRINTS; PR01097; TRNSRECEPTR.  
 CC SMART; SM00248; ANK; 2.  
 CC TIGRFAMs; TIGR00870; trp; 1.  
 CC PROSITE; PS50088; ANK\_REPEAT; 1.  
 CC PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 CC KW Hypothetical protein; Ionic channel; Transmembrane; Ion transport;  
 CC ANK repeat; Repeat.  
 CC FT TRANSMEM 355 375 POTENTIAL.  
 CC FT TRANSMEM 391 411 POTENTIAL.  
 CC FT TRANSMEM 473 493 POTENTIAL.  
 CC FT TRANSMEM 516 536 POTENTIAL.  
 CC FT TRANSMEM 559 579 POTENTIAL.  
 CC FT TRANSMEM 640 660 POTENTIAL.  
 CC FT REPEAT 85 115 ANK 1.  
 CC FT REPEAT 117 141 ANK 2.  
 CC FT REPEAT 163 192 ANK 3.  
 CC FT SEQUENCE 1027 AA; 118101 MW; 81893363A5DE2AD CRC64;  
 CC -----  
 CC Query Match 3.9%; Score 240; DB 1; Length 1027;  
 CC Best Local Similarity 19.5%; Pred. No. 4.2e-08;  
 CC Matches 135; Conservative 109; Mismatches 229; Indels 218; Gaps 26;  
 CC -----  
 CC QY 549 LAACKILKEMSHLETAEEAARAT---REAKYERLALDLFSECYSNSEARAFALLVERNR- 604  
 CC DB 240 LSAFKLSWDLQRLAFEEHEFEKTYLQLSQCKQYSCDLLSQCRSEE--VIAILNKGQNV 297  
 CC QY 605 -----CWS---KTTCLHLATADAKAFPAHDGVQAFTRIWMGDMAAGTPIRLIGA-- 653  
 CC DB 298 NDDNTDVAWSKLSRLKLAIKYEQAQFVSHPHCQQLTSIWY----EGIPYRQSGTWA 353  
 CC QY 654 --FLCPALVYTNLTTFSEAPLRTGLELDLSDLTEKSPLYGL-----QSRVEELVE 705  
 CC DB 354 NFFLYAFLFL-----WPIFCLMYILMPKSRGLRLVR 385  
 CC QY 706 ARAQDRCRAVFLTRWRKFWGAPVTVFLGNVWVYAFLEFLTYLVLVDF----- 757  
 CC DB 386 SP-----FMKFFYSVS-----FATFLGLLTWATEDRYEKGEG 421  
 CC QY 758 ---RPPQPGSGP---EVTLYFWVFTLVLEIRQGFETDTHLVKKFTLYVGDNNWKNCDM 812  
 CC DB 422 GMRASDRGPPATWESLVFTWIGMLWSEIKQLW-----EEGFEYMQWNNWLDLF 473  
 CC QY 813 VAIFLFIWGVTCRMLPSAFE-----AGRTVLAMDVFWVFTLR 848  
 CC DB 474 LMICLYLCISIRL--SAYYIFTYREDPYRYTVTYTSEEPMLVAEALFVGNVFSFAR 531  
 CC QY 849 LHIHFAHQKGLPKIIVWERMMDVFFFLFSLVWLVAVGVTTQALLPHDHDGRLFIFFR 908  
 CC DB 532 ILYFTQNPYLGLQLSUGCNLDVDAKFCFIFVLIISSISGLAQLYWYDNTDVCILPG 591

QY 909 VLKRPYLQIFGQIPLDIDIDARVNCSTHPLL-----EDSPSCPS-LYANWLVILL 958  
 DB 592 ATCKHSSNVFSSI-----ADSYLTLLWSLFSITKPEDTVVVENHKITQWVGQGM 640  
 QY 959 LVTFLLVTVNLLMNLILAMFSYTFQVVGADMEKFORYNL-IVEYHERPALAPPF-IL 1016  
 DB 641 FIMVYHCTSIIVLLNMLIAMSHSQIINDHADLEKFKHRYKLWMAHFDGSSLEPPFNII 700  
 QY 1017 LSHLSL-----TLRRYFKKEA-----EHKREHLER-----DLDPD 1046  
 DB 701 VTPKSLIYVNCLENTVWLLGKTYQKRNRAIIRPGYSRKRNEKSGGHDHDSLKP 760  
 QY 1047 LDQKVVTVETVQ-----KENFLSKMEKRRRDSGEVLRKTAH 1083  
 DB 761 LTVADIITRLVARFIHQTKMKMGVNEDDLHIEIKQDISLRYELDRRRREIVRSSH 820  
 QY 1084 RVDFIAK-----YLGGLRQEKR 1101  
 DB 821 -IDAVKRDIMKMTTSTTSRRPYGGSMRLPKTR 850  
 RESULT 13  
 TRP4\_BOVIN  
 ID TRP4\_BOVIN STANDARD; PRT; 981 AA.  
 AC P79100;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Short transient receptor potential channel 4 (TrpC4) (Capacitative  
 DE calcium entry channel 1) (CCE1).  
 GN TRPC4.  
 OS Bos taurus (Bovinae).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=99113;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RC TISSUE=Adrenal gland, and Retina;  
 RX MEDLINE=97102798; PubMed=8947038;  
 RA Philipp S. Cavalie A., Freichel M., Wissenbach U., Zimmer S.,  
 RA Trost C., Marquart A., Murakami M., Flockerzi V.;  
 RT "A mammalian capacitative calcium entry channel homologous to  
 RT Drosophila TRP and TRPL";  
 RL EMBO J. 15:6166-6171 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BETA).  
 RC TISSUE=Adrenal gland;  
 RX MEDLINE=98158580; PubMed=9498815;  
 RA Freichel M., Wissenbach U., Philipp S., Flockerzi V.;  
 RT "Alternative splicing and tissue specific expression of the 5'  
 RT truncated bCCE 1 variant bCCE 1delta514";  
 RL FEBS Lett. 422:354-358 (1998).  
 CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE  
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A  
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR  
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN  
 CC SHOWN TO BE CALCIUM-SELECTIVE. MAY ALSO BE ACTIVATED BY  
 CC INTRACELLULAR CALCIUM STORE DEPLETION.  
 CC -1- SUBUNIT: ISOFORM ALPHA ASSOCIATES WITH INOSITOL-1,4,5-TRIPHOSPHATE  
 CC RECEPTOR (ITPR). INTERACTS WITH NHERF (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Alpha;  
 CC IsoId=P79100-1; Sequence=Displayed;  
 CC Name=Beta; Synonyms=Delta 514;  
 CC IsoId=P79100-2; Sequence=VSP 006566;  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLAND. LOWER EXPRESSION  
 CC IN HEART AND RETINA. ALSO EXPRESSED IN TESTIS. THE SHORT ISOFORM  
 CC IS SPECIFICALLY EXPRESSED IN THE ADRENAL GLAND.  
 CC -1- SIMILARITY: Belongs to the transient receptor family. Strpc

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CC subfamily.
CC -!- SIMILARITY: Contains 2 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X99792; CAA68125.1; -.
DR EMBL; AJ224862; CAA12161.1; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR002153; Ion_trans.
DR InterPro; IPR004729; Trp_receptor.
DR InterPro; IPR005460; TrpChannel4.
DR Pfam; PF00023; ank; 2.
DR Pfam; PF0520; ion_trans; 1.
DR PRINTS; PR01097; TRNSRECEPTR.
DR PRINTS; PR01645; TRPCHANNEL4.
DR SMART; SM00248; ANK; 2.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS00088; ANK_REPEAT; 1.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Alternative splicing.
FT DOMAIN 1 331 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 332 352 POTENTIAL.
FT DOMAIN 353 364 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 365 385 POTENTIAL.
FT DOMAIN 386 438 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 439 459 POTENTIAL.
FT DOMAIN 460 471 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 472 492 POTENTIAL.
FT DOMAIN 493 513 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 514 534 POTENTIAL.
FT DOMAIN 535 601 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 602 622 POTENTIAL.
FT DOMAIN 623 981 CYTOPLASMIC (POTENTIAL).
FT REPEAT 71 100 ANK 1.
FT REPEAT 143 172 ANK 2.
FT DOMAIN 617 981 BINDS TO ITPR1, ITPR2 AND ITPR3
FT SITE 979 981 (BY SIMILARITY)
FT ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN
FT VARSPLIC 1 513 (BY SIMILARITY).
FT Missing (in isoform Beta).
FT /FTID=VSP_006566.
SQ SEQUENCE 981 AA; 112531 MW; 57B172FD65B791C9 CRC64;

Query Match
Best Local Similarity 3.7%; Score 226; DB 1; Length 981;
Matches 153; Conservative 106; Mismatches 244; Indels 274; Gaps 31;

QY 555 LKEMSHLETE--AEARATREAKYERLALDLFSECVSNSEARAF-----ALLVRRNC 605
D 229 LQELSKVENEPKSEVEELSRQCK--QFADLLDQTRSSRELIILNYRDNLSL--EEOG 284
QY 606 WSKTTLCHLHATADAKAFPHDGVQAFPLRIWGDMA-----AGTPILRLGLAFCLCPA 658
D 285 GNDLARKLKAIRYQKEFVAQPCQQLASRWYDEFFGWRHWAQKMTVCIFVGLFPV 344
QY 659 LVYTNLIITFSEAPLRTGLDQLDLSLTKSPYGLQSRVEELVEAPRAQDGRGPRV 718
D 345 FSVCVLI-----AP-----KSP-LGL----- 359
QY 719 FLLTRWRKFWGAPVTIVLGNVVMYFAFLFLFTYVLL-----VDPRPPQSGSPGV 769
D 360 -----FIRPFKTFICHTASYLTFLFL-----LLLASQHIDRSDLNROGPP--PTIV 406
QY 770 TLYFWVFTLVLEIRQ---GFTTDETHLVKXKFTLYVGNWNKCDMVAIFLFIIVGVTCRM 826

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Db 407 MILPWVGLFIWGEIQKMDGGQLD-----YIHDWNLMDFVMSLVATISLKI 455
QY 827 LP-----SAFE-----AGTVLAMDPMVTLRLIHLFAHKQLGPKLIIVVERNM 870
D 456 VAFVKYSALNPRESWDMHPTLVAEALFAIANIFSRLRISLFTANSHLGPILQISLGRML 515
QY 871 KDVFVFLFSLVMLVAY-----GVTQAL-LPHDGRLEWIFRRVLYRPV 914
D 516 LDILAFLFYICLVLIAPFANGNLQLYFYEEETKGLCKGIRCEKQNNAFSTLP-ETLQSLF 574
QY 915 LQIFGOIPLDEIDAEARVNCSTHPLLEDSPSCPSLYANMLVILLAVTLFLLVNTNLMNLL 974
D 575 WSGIFGLN-----LYVTNVKAQHEFTFVGATMTFTYNNVISLVLLNML 618
QY 975 IAMPSTYTFQVQGNADMFVKFORYMLIVEYHERPALAP-PFILL-----SH 1019
D 619 IAMMNSYQLIADHADIEMKFARTKLMWSYFEGGTLPFTFNVIPSPKSLWYLKIKWIWTH 678
QY 1020 L-SLTLR-----VFKEAEH-KREHLERDLPDLDOKV-----TWETVOKENF 1062
D 679 LCKKVRKXPFSEFGTIGRAADNLRHHOYQEWENLVKRYVAAMTRDAKTEGLTEENF 738
QY 1063 -----LSKMEK-----RRRDEG----- 1075
D 739 KELQDISFRFVGLLRLGSLKSTVQSAQGTKESSNSADSDEKSDNEGSKDKKNFSL 798
QY 1076 -----EVLKTAHVDFIA--KYLGGIREQEKRIK 1103
D 799 FDLTLIHPRSAIAAERHTISNGSALVQVEPPREKQKVNFTDIRHGLFHRRSKQHA 858
QY 1104 CLESQINVCSLVSSVADVLAQCGGPRSQ-----HCGEGSQLVAADR 1147
D 859 AAEQANQIFSVEGVARQQAEGPLERSIQLERSLASRGDLNIPGLSEQCILVDHR 915

RESULT 14
TRP4 HUMAN
ID TRP4 HUMAN STANDARD; PRT: 977 AA.
AC Q9UBN4; Q15721; Q9UBI0; Q9UBI1; Q9UBI2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Short transient receptor potential channel 4 (trpC4) (trp-related protein 4) (htrp-4) (htrp4).
GN TRP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Kidney;
RX MEDLINE=20498755; PubMed=11042129;
RA McKay R.R., Symczek-Seay C.L., Lievrement J.-P., Bird G.S., Zitt C., Juengling E., Lueckhoff A., Putney J.W. Jr.;
RT "Cloning and expression of the human transient receptor potential 4 (TRP4) gene: localization and functional expression of human TRP4 and TRP3.";
RL Biochem. J. 351:735-746 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA; DELTA AND GAMMA).
RC TISSUE=Embryonic kidney;
RX MEDLINE=21099836; PubMed=11163362;
RA Mery L., Magnino F., Schmidt K., Krause K.-H., Dufour J.-F.;
RT "Alternative splice variants of htrp4 differentially interact with the C-terminal portion of the inositol 1,4,5-trisphosphate receptors.";
RL FEBS Lett. 487:377-383 (2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX MEDLINE=21671347; PubMed=11713258;
RA Schaefer M., Plant T.D., Stresow N., Albrecht N., Schultz G.;
RT "Functional differences between TRPC4 splice variants.";

```





QY 1063 -----LSKMEK-----RRDSEG----- 1075  
 Db 737 KELKQDISSFRFEVLGLLRSSKSLTQSANAKESSNSADSDSEKSGNKKXNFSL 796  
 QY 1076 -----EVURKTAHRVDFTAKYLG-GLRQEKRIKC 1104  
 Db 797 FDLTTLHPRSAIAIABERHNISNGSALVQEPPEKQKQKVFVTDIKNFGLFHRRSKQNA 856  
 QY 1105 LESQINVCVLSVADVLVLA--CGGGP--RSSQHCGE-----SOLVAADHR 1147  
 Db 857 AEQNAQ-----IFSVSEVARQAAGLEPLRNQIESRGLASRGDLIPGLSEOCVILVDHR 912

RESULT 15  
 TRP4 MOUSE  
 ID TRP4\_MOUSE STANDARD; PRT; 974 AA.  
 AC Q9QU05; Q62350; Q9QU09; Q9QZC0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Short transient receptor potential channel 4 (TrpC4) (Receptor-  
 activated cation channel TRP4) (Capacitative calcium entry channel  
 TRP4).  
 GN TRP4 OR TRRP4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC TISSUE=Brain;  
 RA Zhu X., Boulay G., Jiang M., Birnbaumer L.;  
 RT "Trp4 is involved in capacitative calcium entry in murine cells.";  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC TISSUE=Brain;  
 RA Qian F., Philipson L.H.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC TISSUE=Brain;  
 RX MEDLINE=98171352; PubMed=9512398;  
 RA Mori Y., Takada N., Okada T., Wakamori M., Imoto K., Wanifuchi H.,  
 RA Oka H., Oba A., Ikenaka K., Kurosaki T.;  
 RT "Differential distribution of TRP Ca2+ channel isoforms in mouse  
 brain.";  
 RL NeuroReport 9:507-515(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RX MEDLINE=20545496; PubMed=10980202;  
 RA Tang Y., Tang J., Chen Z., Trost C., Flockerzi V., Li M., Ramesh V.,  
 RA Zhu M.X.;  
 RT "Association of mammalian trp4 and phospholipase C isozymes with a PDZ  
 domain-containing protein, NHERF.";  
 RL J. Biol. Chem. 275:37559-37564(2000).  
 RN [5]  
 RP SEQUENCE OF 505-642 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=96003894; PubMed=7575478;  
 RA Petersen C.C.H., Berridge M.J., Borge M.F., Bennett D.L.;  
 RT "Putative capacitative calcium entry channels: expression of  
 RT Drosophila trp and evidence for the existence of vertebrate  
 RT homologues.";  
 RL Biochem. J. 311:41-44(1995).  
 RN [6]  
 RP FUNCTION.  
 RX MEDLINE=21113116; PubMed=11175743;  
 RA Freichel M., Suh S.H., Pfeifer A., Schweig U., Trost C.,  
 RA Weissgerber P., Biel M., Philipp S., Freise D., Droogmans G.,  
 RA Hofmann F., Flockerzi V., Nilius B.;  
 RT "Lack of an endothelial store-operated Ca2+ current impairs  
 RT agonist-dependent vasorelaxation in TRP4-/- mice.";  
 RL Nat. Cell Biol. 3:121-127(2001).

CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE  
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A  
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR  
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN  
 CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE  
 CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION. TRPC4  
 CC DEFICIENT MICE LACK A STORE-OPERATED CALCIUM ENTRY IN ENDOTHELIAL  
 CC CELLS.  
 CC -!- SUBUNIT: ISOFORM ALPHA BUT NOT ISOFORM BETA ASSOCIATES WITH  
 CC INOSITOL-1,4,5-TRIPHOSPHATE RECEPTOR (ITPR) (BY SIMILARITY).  
 CC INTERACTS WITH NHERF.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Alpha;  
 CC IsoId=Q9QU05-1; Sequence=Displayed;  
 CC Name=Beta;  
 CC IsoId=Q9QU05-2; Sequence=VSP\_006570;  
 CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN BRAIN (HIPPOCAMPAL CA1  
 CC PYRAMIDAL NEURONS, DENTATE GYRUS GRANULE CELLS, AND CEREBRAL  
 CC CORTICAL NEURONS, AND IN THE SEPTAL NUCLEI AND THE MITRAL LAYER OF  
 CC OLFACTORY BULB). LOWER LEVELS ARE DETECTED IN OTHER TISSUES.  
 CC -!- SIMILARITY: Belongs to the transient receptor family. StrpC  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 2 ANK repeats.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AF011543; AAD10167.1; -.  
 CC EMBL; U50922; AAC05179.1; -.  
 CC EMBL; AF190646; AAF01469.1; -.  
 CC EMBL; U50921; AAC05178.1; -.  
 CC EMBL; AF019663; AAD10168.1; -.  
 CC EMBL; X90697; CAA62230.1; -.  
 CC PIR; S59128; S59128.  
 CC MGI; MGI:109525; TrpC4.  
 CC InterPro; IPR002110; ANK.  
 CC InterPro; IPR002111; Cat channel\_TrpL.  
 CC InterPro; IPR005821; Ion\_trans.  
 CC InterPro; IPR002153; Trans\_receptor.  
 CC InterPro; IPR004729; Trp\_CaChannel.  
 CC InterPro; IPR005460; TRPChannel4.  
 CC Pfam; PF00023; ank; 2.  
 CC PRINTS; PR01097; TENSRECEPTP.  
 CC PRINTS; PR01645; TRPCHANNEL4.  
 CC SMART; SM00248; ANK; 2.  
 CC TIGRFAM; TIGR00870; trp; 1.  
 CC PROSITE; PS50088; ANK\_REPEAT; 1.  
 CC PROSITE; PS0297; ANK\_REPEAT; 1.  
 CC Ionic channel; Transmembrane; Ion transport; Calcium channel;  
 CC ANK repeat; Repeat; Alternative splicing.  
 KW DOMAIN 1 329 CYTOPLASMIC (POTENTIAL).  
 KW TRANSMEM 330 350 POTENTIAL.  
 FT DOMAIN 351 362 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 363 383 POTENTIAL.  
 FT DOMAIN 384 436 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 437 457 POTENTIAL.  
 FT DOMAIN 458 469 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 470 490 POTENTIAL.  
 FT DOMAIN 491 511 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 512 532 POTENTIAL.  
 FT DOMAIN 533 599 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 600 620 POTENTIAL.  
 FT DOMAIN 621 974 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 69 98 ANK 1.  
 FT REPEAT 141 170 ANK 2.

Search completed: September 14, 2004, 00:04:52  
Job time : 24 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 14, 2004, 00:02:13 ; Search time 26 Seconds  
(without alignments)  
4310.120 Million cell updates/sec

Title: US-10-026-188-8

Perfect score: 6093

Sequence: 1 MQDVQPRPGSPGDAEDRE.....HRGLDWEQPGAGQPPSDT 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1134.5	18.6	488	2 JCY7995	transient receptor
2	1070.5	17.6	1868	2 T23707	hypothetical prote
3	1000	16.4	1400	2 T22644	hypothetical prote
4	889	14.6	1707	2 T18951	hypothetical prote
5	326.5	5.4	1275	2 JU0092	trp protein - frui
6	317.5	5.2	1274	2 JN0015	trp protein - frui
7	294	4.8	1418	2 S40764	hypothetical prote
8	266.5	4.4	1124	2 JH0588	calmodulin-binding
9	247	4.1	899	2 F88391	protein R06B10.4 [
10	235.5	3.9	823	2 S44873	ZC21.2 protein - C
11	192	3.2	828	2 JC5807	trp3 protein - rat
12	176.5	2.9	793	2 S68238	trp-1 protein - hu
13	176.5	2.9	810	2 T38361	TRPC1 protein - hu
14	165	2.7	823	2 T34472	hypothetical prote
15	164.5	2.7	3678	2 S28916	dystrophin - mouse
16	160.5	2.6	482	2 S61648	probable membrane
17	146	2.4	725	2 JC7531	calcium transport
18	145.5	2.4	675	2 T20822	hypothetical prote
19	144.5	2.4	839	2 JC7621	capsaicin receptor
20	139	2.3	727	2 JC7796	epithelial calcium
21	132	2.2	790	2 T20312	hypothetical prote
22	130	2.1	838	2 T09054	hypothetical prote
23	130	2.1	2049	2 T43161	sodium channel pro
24	128	2.1	723	2 JC7795	epithelial calcium
25	128	2.1	900	2 T33026	hypothetical prote
26	124.5	2.0	608	2 G02640	polycystic kidney
27	123.5	2.0	1199	2 T37561	probable transcrip
28	123	2.0	160	2 S63993	acrosomal protein
29	123	2.0	1075	2 T45570	kinesin-like prote

#### RESULT 1

JCY7995

transient receptor potential-melastatin 4 channel - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-Nov-2003 #sequence\_revision 10-Nov-2003 #text\_change 24-Nov-2003

C;Accession: JCY7995

R;Murakami, M.; Xu, F.; Miyoshi, I.; Sato, E.; Ono, K.; Iijima, T.

Biochem. Biophys. Res. Commun. 307, 522-528, 2003

A;Title: Identification and characterization of the murine TRPM4 channel.

A;Reference number: JCY7995; PMID:12893253

A;Accession: JCY7995

A;Molecule type: DNA

A;Residues: 1-488 <MUR>

A;Cross-references: GB:NM000319

A;Experimental source: Brain, C57/BL6

C;Comment: This protein, a member of subfamily of transient receptor potential channels,

C;Genetics:

A;Gene: trpm4

A;Map position: 7B2

A;Introns: 12/2; 153/2; 197/3; 256/1; 315/2; 384/1; 428/2; 452/3

C;Keywords: calcium entry; transient receptor potential; transmembrane domain; TRPM

Query Match 18.6%; Score 1134.5; DB 2; Length 488;

Best Local Similarity 47.6%; Pred. No. 1.1e-74;

Matches 236; Conservative 72; Mismatches 123; Indels 65; Gaps 10;

QY 704 VEAPRAQDGRGPRVAF--LLTRWRKFWGAPVTVFLGNVVMYPAFLFLEYVLLVDFRPP 760

Db 20 VALERRQRRPGRCALCCGKFSKRWSDFGAPVTAFLGNVSVLLFLLFAHVLVDFQPT 79

QY 761 PQGPGSPVTLFWVFTLVLEIRQGF-----FTDEDTHLVKFTLYVGNWNK 809

Db 80 K-PSVSELLLYFWAFTLLCEELQGLGGWGLASGGRGDPDRAPLRHLHLVLSDTNQ 137

QY 810 CDWVAFLFIVGVTCTRMPLSAFEAGRTVLAMPDFMTLRLLHFAHKGQPKIIVVERM 869

Db 138 CDLLALTCELVGGGRITPGLDGLRTVLCCLDFMLFTLRLLHFTVVKQGPRIIVSKM 197

QY 870 MKDVFFFLFSLVWLVAYGVTTQALLHPHDGRLWIFRRVLXPYLIQIFQPLDIDEA 929

Db 198 MKDVFFFLFCLVWLVAYGATEGILRPQDRSLPSLRRVFPYLIQIFQIPQEMDVA 257

QY 930 RV---NCS-----THPLLEDSF---SCPSLYANWLVLLVTLVTLVNNLLMIAM 977

Db 258 LMPGNCNMGERSWAHP-----EGPVAGSCVSYANWLVLLVTLVTLVNNLLMIAM 313

QY 978 FSYTFQVQGNADMFWKFORYNLIVEYHERPALAPFPILLSHLSLTLR-----RVFK 1029

Db 314 FSYTSKVHNSDLTWAKQRYSLIRFHSRPAAPLIITISHVRLDLKMRRCRRAN 373

QY 1030 KEAEKREHLERDLDPDLQKVVTWETQKFNFLSKMEKRRRDSGEVLKTAHRVDFIA 1089

Db 1030 KEAEKREHLERDLDPDLQKVVTWETQKFNFLSKMEKRRRDSGEVLKTAHRVDFIA 1089

#### ALIGNMENTS

sodium channel pro  
hypothetical prote  
dystrophin, muscle  
beta spectrin, bet  
olfactory channel  
hypothetical prote  
probable non-ribos  
hypothetical prote  
bimD protein - Eme  
protein B0212.5 [1  
sodium channel pro  
fodrin alpha chain  
calcium channel al  
calcium channel al  
trp-like protein -  
ring finger B-box

30 123 2.0 2019 2 A33996  
31 122.5 2.0 2322 2 T10542  
32 122.5 2.0 3685 1 A27605  
33 121.5 2.0 2388 2 JE0271  
34 121 2.0 937 2 T37241  
35 121 2.0 1657 2 T15838  
36 121 2.0 5149 2 F83345  
37 120.5 2.0 854 2 T23155  
38 120.5 2.0 1506 2 S52957  
39 119 2.0 957 2 D88651  
40 118.5 1.9 2016 2 A38195  
41 117.5 1.9 2472 2 A35715  
42 116.5 1.9 1559 2 T30535  
43 116.5 1.9 1687 2 S41742  
44 116 1.9 149 2 S59129  
45 116 1.9 638 2 JC7753

Db 374 LPASPVFEHFVCLSKAEKRLTWESVHKENFLIAQARDKRDSDSERLKRKTSQKVDTAL 433  
 QY 1090 KYLGLEOEKRIKLESIQVSVLVSSVADVLQAQGGPRSSQHCGBGSQVLAADHRGG 1149  
 Db 434 KQLQIRYDRRLGLEREVOHCRLVTWBAALSH-----SALL----- 473  
 QY 1150 LDGWEQPGAGQPPSDT 1165  
 Db 474 -----PPGAPPPPSPT 484

RESULT 2  
 T23707  
 hypothetical protein T01H8.5 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T23707; T24342  
 R:Kerhaw, J.  
 submitted to the EMBL Data Library, November 1996  
 A:Reference number: Z19786  
 A:Accession: T23707  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1868 <W1L>  
 A:Cross-references: EMBL:Z83117; PIDN: CAB05572.1; GSPDB: GN00019; CESP: T01H8.5  
 A:Experimental source: clone M04C7  
 R:Lennard, N.  
 submitted to the EMBL Data Library, September 1996  
 A:Reference number: Z19877  
 A:Accession: T24342  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1868 <W12>  
 A:Cross-references: EMBL:Z80219; PIDN: CAB02303.1; GSPDB: GN00019; CESP: T01H8.5  
 A:Experimental source: clone T01H8  
 C:Genetics:  
 A:Gene: CESP: T01H8.5  
 A:Map position: 1  
 A:Introns: 24/3; 112/3; 191/3; 220/1; 268/2; 375/2; 456/2; 552/3; 625/2; 744/3; 850/2; 1

Query Match 17.6%; Score 1070.5; DB 2; Length 1868;  
 Best Local Similarity 24.5%; Pred. No. 3.9e-69;  
 Matches 343; Conservative 231; Mismatches 486; Indels 341; Gaps 41;

QY 26 GEVNF -GGSGKRGKFPVPSVLFDFLLAEWHLPAPNLVSVLVEGEEPPFAMKSWL 84  
 Db 214 QGVFQGGPHYKAYVRVNFDEPAYIMSLFEHWQISPPRLIITVHGTSNFDLPKL 273  
 QY 85 RDVLRKGLVKAQSTGAMILTALRVGLARHVQAVRDHSLASTSTKVRVAVAGASLGR 144  
 Db 274 ARVFRKGLLKAATTCAMITTSCTGTGVVHVAAALEG---AQSAQRNKIVGIGIAPWG- 329  
 QY 145 VLHRLILEAODEF-----PVHYEDDGGSGPLCLSDSNLSHFILVEPFGPGKDGLT 198  
 Db 330 -----LUKREDFTGQDKTVPIYP-----SSSGRFTGLNRRHSYFLLVDNVTGVRIGAEV 380  
 QY 199 ELRLRKHISQRAQYGGTGIPIVLCILVNGDPNTERISRAVEQA--APWLILVGS 256  
 Db 381 ILRKLWYISQKIFGTR--VPVVCVLEGGSTIRSVLDVTVNVPRVPVVCVGS 438  
 QY 257 GGIADVLAL-----VNPHLL-----VPKVAEKOFKFPKHSFSDIVRTWTKLQNI 306  
 Db 439 GRAADLLAFHQNVTEGGLPDIRQVRLVLTFTFGSEAAH-----RLHLEL 488  
 QY 307 T---SHQHLTVDYDEQSEELDTVLKALVKACKSHSQEPQDYLDELKLAVALVDVDI 363  
 Db 489 TVCAQHKLLTIFRLGEQGEHVDHALTLKLG-----QNLSDAQALALANRVDI 542  
 QY 364 AKSEIFNGDVEMVSCDLEEVMDALVSNKPEFVRFLVNGADVADFLTVGRLOELY---- 419  
 Db 543 ARSDVFMGHEWFPQAALHNAMMEALTHRDVDFVRLLEQGINNQKFLATISRLDELNTDK 602  
 QY 420 -----RSVSRK-----SLFLDLL-----QRKQEEARL- 441

RESULT 3  
 T22644  
 hypothetical protein F54D1.5 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

Db 603 GPPNTLFYVRDVVRVQGYRFLKPLDIGLVIEKLMGNSYQCSYTTSEFRDYKORMKRVK 662  
 QY 442 -----TLALGTQOARE-----PPAGPEA-F 461  
 Db 663 HAQKAMGVSSRRSRPTGSGIASQSTEGMGVGGSSVAGVFGNSFGNQDPLDPHVR 722  
 QY 462 SLHEVSRVLKDFL--QDACRGFYQDPRGDRRAEKGAKRPTQKQWLLDNQKSEN--- 516  
 Db 723 SALSGSRALSNHILWRSAFRGNF---PANDMRPNLGDSDCSEFDEELSLTSASDGS 778  
 QY 517 -----PWEDLFLWAVLQNRHEMATYFWAMGCEGVAALAAACKILKEMS-----HLE 562  
 Db 779 QTEPDFRYPYSELMIWAVLTKRQDMAMCMWQHGEAMAKALVACRLYKSLATEAADYLE 838  
 QY 563 TEAEARATREAKYERIALDLFSYCSYNSSEARAFALLVRNRKWSKTKTCLHATEADAKA 622  
 Db 839 VEICEELKYAEPRILSLELLDHCYHVDDAQTQLLYELSNWSNETICLALAVVNNKH 898  
 QY 623 FFAHGDGVQAFLTRIWMGDMAAGT--PIRLRLGAFICPALIV----- 660  
 Db 899 FLAHPCCQIILLADLWHGGLRMRTHSNIKVVLGLICPPFIQMLEFKTREELNQPTAAEH 958  
 QY 661 -----YTNLIITFSSEAPLRTGLELDQLDLSLDT----- 689  
 Db 959 QNDMNYSS 1018  
 QY 690 ----- 689  
 Db 1019 LFHSRRRKAKKNEKCDRETASACEAGNRQIQNGGLTAETGYTFGBESNGVSPPPVYMRANS 1078  
 QY 690 -----KSPYGLQSRVEELVEAPQOQDR-----GPAVLELLTRWRKFW 728  
 Db 1079 RSYNNRSDMSKTSVIFGSDPNLSKLOKSNITSTDRPNPMEQFOGTRKIKRRRFFYEF 1138  
 QY 729 GAPVTFLGNVVMYFAELFLEYVLYVDFRPPQSGPVEYTLVFWVTLVLEIRQGF 788  
 Db 1139 SAPISTFMSWTISFILFTFTFTYLLV--KTPPR-PTVIEYLIAVAAFGLEQVRKLI 1195  
 QY 789 TDETHLVKTKTLVGVGNWNNKCDVVAIFLFTVGVTCRMLPSAFAGRTVLAMDFMVFILR 848  
 Db 1196 SDARP-FYEKIRTYVCSFVNCVTILAIIFYIVGFMRFCGVS-AVGRVILACDSVLWTMK 1253  
 QY 849 LIHFAIHKQGLKPIIVVERMMKOVFPFLFSLVWLVAIVTQTALLHPHGRLEWIP-R 907  
 Db 1254 LLDYMSVHPKLGYPVTWAGKMIQNSYIIVMLVLTLLSFGLARQCSITYP-DETWHILVR 1312  
 QY 908 RVLVRPYLQIFGOPLDEIDEARVNCSTH-----PLLEDSP---SCPSLYANWL 954  
 Db 1313 NIFUKPYFMYGEVYADRID---TCGEANDQHLNGLGPPVILGNGTGLSCVPGY--WI 1366  
 QY 955 VILLIVTLLVNTVLLNMLLIAMFSYTFQVQGNADMFEWFKQRYNLIVYEHHERPALAPPF 1014  
 Db 1367 PPLMTFPELLIANILLMSMLIAFNHIDATDKSQIWLFRQYKQVMEYSTPLPPLP 1426  
 QY 1015 ILLSHSLTLRRVPKKEAEHREH-----LERDLPDLQDKVVTWETVQKENFL-S 1064  
 Db 1427 TPLVHGVILQIFVTRLSKCSQERNPILLKIAELFLDNQIEKHLDFEEDCMEDLARQ 1486  
 QY 1065 KMEKERRDSEGEVLKRTAHR-----VDFIAKYLGG---LREQSKRIKLESQINYCSV 1114  
 Db 1487 KLNKNTNEORILRADIRTDQILNRLDLQAKESMGDRVDINDVESRLASVEKAQN---E 1543  
 QY 1115 LVSSVADVLQAQGGPRSSQHC 1135  
 Db 1544 ILECVALLNQNAFTAIGRC 1564

C:Accession: T22644  
R:Lennard, N.  
Submitted to the EMBL Data Library, July 1996  
A:Reference number: Z19592  
A:Accession: T22644  
A:Status: preliminary; translated from GB/EMBL/DBBJ  
A:Molecule type: DNA  
A:Residues: 1-1400 <WIL>  
A:Cross-references: EMBL:Z77132; PIDN:CAB00861.1; GSPDB:GN00022; CESP:F54D1.5  
A:Gene: CESP:F54D1.5  
A:Map position: 4  
A:Introns: 21/2; 51/2; 205/2; 276/3; 364/2; 466/3; 507/3; 536/3; 599/3; 672/2; 699/3

Query Match 16.4%; Score 1000; DB 2; Length 1400;  
Best Local Similarity 27.8%; Pred. No. 3.5e-64;  
Matches 335; Conservative 204; Mismatches 478; Indels 188; Gaps 46;

QY 26 GEVNF-GSGKRGKRVFVPSGVAPSVLFDLLAEWHLPAPNLVSLVSGEEQPFAMKSWL 84  
DB 151 GTIVFGGAHAHAQVRLSYDSEPLDVYMLMEKVMGLEAPRLVITVHGMNFLEERL 210  
QY 85 RDVLRKGLVKAQSTGAWILTSALRVGLARHYQAVRDHSLASTSTKVRVAVGWSLGR 144  
DB 211 GRLFRKGLKAAQTTCGAWIITSGLDGSGVVRHAKAL-DEAGISARMSRQIVTIGIAPWGV 269  
QY 145 VLHRRILEBAQEDFFVHYPEDDGGSGPLCSLDSNLISHEILVPEPPGKGDGTELRLRL 204  
DB 270 IRRKRLIRONEH--YYVDHSLSVNANVGIILNDRHSYFLLADNGTVGRFGADLHLRQNL 327  
QY 205 EXHISEQRAGYGGTGTIEIPVLCILVNGDPNTERISRAV--EQAAPWILVSGSGIADV 262  
DB 328 ENHI-----ATFGNGR-KVPVVCTLLEGISINAHIDVYTMKPDIPALVCDGSGRAADI 382  
QY 263 L---AALVNQPHLLVPKVAEK--OPKEKPPSKHFSWEDIVRTWKLLQNITSHQHLLTVY 316  
DB 383 ISFAARYINSQDTFAAEVGEKRLNLIKMFVPEP--DQEMFR--KITECVI-RDILLRIF 437  
QY 317 DFEQEGSELDVILKALVKACKSHSQEPQDYLDELKLAANDRVDIKSEIFENGVEWK 376  
DB 438 RYQGEEDVDVFLITVLTQ---KNLPPD--EQALTLTWNVRDLAKSLCFSNGRKWS 491  
QY 377 SCDLSEVMVDALVSNKPEFVRLVNDGADVFLTYGRLOELY-----RSVSRKSL 428  
DB 492 SDVLEKANDALYWDVDFVECLLENGVSKNFLSINRLENLYNMDINSASVVRNWMEN 551  
QY 429 FDLQRKQEBEARTLAGLTOQAREPPAGPAPFSLHEVSRLVKDFLODACRGFYQDGRPG 488  
DB 552 FDSM---DPHTYLTIPMIG-QVVEKLMG-NAFQLYTTSRSEK-----GKYD 592  
QY 489 DRRRAEKGP--AKRPTGOKWLL-----DLNQKSEN-----PWRDLFLMAVLQNRHEM 533  
DB 593 RYKRINQSSYFHRKRVKIVQKELFKKSDQDQINDNEEDFSFAYFPNDLLIWAFLTSRHGM 652  
QY 534 ATYFWAMGEGVAAALAAKILK-----EMSHLETEAARATREA-KYERLALDLFSE 586  
DB 653 AECWVHGEDAMAKCLLRLYKATAKIAEDYLDVE-EAKRLFONAVKREDALIELLDQ 711  
QY 587 CYSNSEARAFALLVRNRNCRWTKTCLHATEADAKAFFAHGQVQAFLETRIMWGM--AAG 644  
DB 712 CYRADHRTLRLLRMLPWHGNNCLSLAVANTKTFLAHPCCQILLAEHLHGSLKVRSG 771  
QY 645 TPILRLIGAFIC-PALVY-----TNLITSEAPLTGLEDL-QDLDSLDTEKSPLY 694  
DB 772 SNV-RVLTALICPPALLFWAYKPKHSKTRALLSEETP-----EQLPYPRESITTSNRY 825  
QY 695 GLQSRVEELVEAPRAOG-----DRCPRAVE-----LLTRWPK 726  
DB 826 RYSGKEEQKETLLEKSTYKVTIISRSKNSGVASVYSGASMMKRPQNLKPERFRA 885  
QY 727 FWGAPVTVFLGNVVMYFAFLFLFTYVLLVDPRPPQPGSGPEVTLTYFWVFTLVLEIROG 786  
DB 941

886 FYSSPITRFSWSCIATLFLTTQTICILLE---TSLKPSKYEWITFTVTTLSVEHIRK- 941  
QY 787 FETDEDTHLVKFTLYVGDNNKCDMVALFPIVGTCTMLPSAFEA-GRTVLAMDWFVYF 845  
DB 942 LMTSEGSINEKVKVYAKWYNITWTSALLPFLVGVGFLVPMYRHSWGRVLLSPSNVLF 1001  
QY 846 TURLIHIFAIHQKQPKIIVVERMMKDVFFFLFSLVMLVAYGVTTQALLHHPDGLLEWI 905  
DB 1002 YMKIFEYLSVHPHLLGPYIQMAAKWMSYICVLLVPLMAFGVNRQALTEPNVKDWHML 1061  
QY 906 F-RVLYRYPYQIQFQIPDEIDARVNCSTHPLLEDSPCSPSLYANWLVILLVTFLL 964  
DB 1062 LVNRNIFKYPFMYGEVYAGEID---TCG-----DEGIRCFPGY--PIPLLWVIFLL 1109  
QY 965 VTNVLLMNLITAMESYTTQVQGNADMEFWKFORYNLIVYHERPALAPPEILLSHL--- 1020  
DB 1110 VANILLULLLTAIFNNIYNDISIEKKEIWLFOYQOLMEYHDSPLPPFPSTFAHYHYFI 1169  
QY 1021 --SLTRRVFKK-----EAEHKKR-EHLERDLPDQKVVETWQKENFSL 1064  
DB 1170 DYLYNLRPRDITKRFRSEHSIKLSVTEDEMKRQDFFEDCIDLTR-----IRK---L 1218  
QY 1065 KMEKRRRSEGEVLKRTAHRV-----DPIAKYGLGLREQEKRIKLESQINYSVLVSS 1118  
DB 1219 KLNTKEPLSVTDLTCLTCQVRHDLMQENFLK-----SRVYDIETKIDHISNDSDE 1269  
QY 1119 VADVL 1123  
DB 1270 VVQIL 1274

RESULT 4  
T18951  
Hypothetical protein C05C12.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T18951  
R:White, S.  
Submitted to the EMBL Data Library, January 1996  
A:Reference number: Z19050  
A:Accession: T18951  
A:Status: preliminary; translated from GB/EMBL/DBBJ  
A:Molecule type: DNA  
A:Residues: 1-1707 <WIL>  
A:Cross-references: EMBL:Z68333; PIDN:CAA92726.1; GSPDB:GN00022; CESP:C05C12.3  
A:Experimental source: clone C05C12  
C:Genetics:  
A:Gene: CESP:C05C12.3  
A:Map position: 4  
A:Introns: 13/3; 52/1; 82/3; 100/3; 174/3; 203/1; 249/2; 292/1; 358/2; 406/2; 436/2; 477/2; 542/3; 1595/1; 1647/2; 1673/3; 1695/3

Query Match 14.6%; Score 889; DB 2; Length 1707;  
Best Local Similarity 22.3%; Pred. No. 6e-56;  
Matches 308; Conservative 229; Mismatches 456; Indels 390; Gaps 43;

QY 26 GEVNF-GSGKRGKRVFVPSGVAPSVLFDLLAEWHLPAPNLVSLVSGEEQPFAMKSWL 85  
DB 197 GNIVFEGTA-HHAQYARISFSDSDPRDIVHLMKMKWKLKPKKLITTINGLTKFDQPKLA 255  
QY 86 DVLRLKGLVKAQSTGAWILTSALRVGLARHYQAVRDHSLASTSTKVRVAVGWSLGRV 145  
DB 256 RFRKRGIMKIATKSTDAWIITSGLDGSGVVKHLDLSALHDH--GNHTSKNHVVAIGIASWGL 313  
QY 146 LHRILEBAQEDFFVHYPEDDGGSGPLCSLDSNLISHEILVPEPPGKGDGTELRLRL 205  
DB 314 KQRS--RFVGKDSVTYATNVFNNT-RLKELNDNHSYFLSDNGTVNRYGABIIMRKRL 370  
QY 206 KHISEQRAGYGGTGTIEIPVLCILVNGDPNTERISRAVE--QAAPWILVSGSGIADV 263  
DB 371 AYLAQ-----GDKKRSALPLVCVLEGGAFITKVDHYVTTIPRIPVIVCDGSGRAADIL 425  
QY 264 A-----ALVNQPHLLV---PKVAEQKFKFKFSKHSWEDIVRWTKL 302

Db 426 AFAHQAVSQNGFLSDNIRNQLVNIVRIFGVDPKTAQKLIQK----- 467  
Qy 303 LONITSHOHLTVYDFEGSEELDTVILKALVACKSHSQBPQDYLDLKLAVANDRVD 362  
Db 468 IVECTNKSMTIIFRLGESSREDLHVIMSCLL---KQNLSP---EQQLALANRAD 521  
Qy 363 IAKSEIFNGDVEWKSCLDEEVVMDALVSNKPEFVRLFVDNGADVADFLTYGRLOELY--- 419  
Db 522 IARTEIFANGTEWTQDLHNAMIBALSNDRIDFVHLLLENGVSMQKFLTYGRLEHLYNTD 581  
Qy 420 ---RSVRSKSLLLFDLQKQBEARLTLAGLGTQQAAREPPAPFAPSLHEVSRVLKDFIQD 476  
Db 582 KGPQNTLRNLLVDSKHH-----IKLVEVGRLVENLMGN 615  
Qy 477 ACRGFYQD-----GRPDREAEK----- 495  
Db 616 LYKSNYTKBEFKNQYFLPNRRKQFGKRVHSNNGRNDVIGPSGDAGRSMSSQWISLIN 675  
Qy 496 -----GPAKPTGQKWLDDLNQKSEN-----PWRDLFWAVLQNRHEMATY 536  
Db 676 NARNSIISLFGGGRKRESDEDDPSNLEBANMDFTERYPYSDLMIAVLTAKQMAKL 735  
Qy 537 FWAMQOEVAAALACKILKEMSHLETEAARATREA-----KYERLALDLFS 585  
Db 736 MWTHGEGMAKALVASRL-----YVSLAKTASLATGEICMSQDFTFEFSSELAVEVLE 790  
Qy 586 ECVNSEARAPALLVRRNRKSKTKTCLHLATEADAKAFPAHDGVAQLFTRIWMGDMA--- 642  
Db 791 YCTKHGRDQTLRLTCELANGWDETCLSLANNNGHKKFLAHPCCQMLLSLWQGLLMKN 850  
Qy 643 -AGTPILRLLAGFLCPALVYNTLITFSBEAPLR-----TG 676  
Db 851 NQNSKVLTCCLAA---PPLIF---LLGFKTKQQLMLQPKTAAEHDEMSDSEMSAEDTDT 905  
Qy 677 LEDQLDLSLTE-----KSPLYGLOSREVELVEA 706  
Db 906 SDSSSDSDSDDEDAKLAQSLASADQPLSIHRLVRDKLNFSEKKPDNG---ISRIYVA 961  
Qy 707 P-----RAQ----- 710  
Db 962 PPVITGRNARTMSIKKSKKVIKPPACKLKIETSDDDDEQOKKATEMCKSTFFDFDFF 1021  
Qy 711 -----GDRGPRAV-----FLITR-----WRK 726  
Db 1022 YINRTGKGSVAVAMNHDDVIDPSEELDTQTRKSSREFSSRNVTYQVYTORLSWK 1081  
Qy 727 ---FWGAPVTVFLGNVNYFA---FLFTFYVLLVDFRPPPGSPGSEVTLYFWVFTLV 779  
Db 1082 KIMBFYKAPITTYW---LWFFAFIWFLLITLNLVKTQ---RIASNSEWYVYFAYT 1135  
Qy 780 LE---EIRQGFPTDTHLVKKFTLYVGDNNWKNCDMVAIFLFIQVTCRMLPSAFAEGR 836  
Db 1136 LEIGRKVVSTTMDTSKEVLKQLRVFPFYQYRNGLLAFGLLYLIAYFIRLFTTKLGR 1195  
Qy 837 VLAMDFWVFTLRLIHI FAHKOLGPKIIVVERMMKDVFFFLFSLVNLVAYGVTTQALLH 896  
Db 1196 LIICNSVITWSLKLVDYLSVQOGLGPIYINVAEMIPTMPLCVLVTILYAFGLLRQSTY 1255  
Qy 897 PHDGRLEW---IFRVLVRPYLQIFGOIPLEIDEARVNCSTHPLLLSDSPSCSLYAN- 952  
Db 1256 PYE---DWHVILVRNIFIQPFMYLGEVYAAEID---TCGDEIWTQTHEDENIPISMLNV 1308  
Qy 953 -----WLVIILLVFLVTVNLLNMLIAMPSTYFQV---VQGNADMFWKFORYNLIV 1002  
Db 1309 THECTVPGYWIAPVGLTVFMLATNVLNVMVAGCTYIFEXHIOSTRIF-LFERYGQVM 1367  
Qy 1003 EYHERPALAPPILLSHLSLTLRRVFKKBAEHRHL-ERDL-----PDLDQKVVTWET 1056  
Db 1368 EYESTPWLPPPTTIIYHVIWLFKLTKSSSRMFERKNLFDQSLKPLSPDEM-EKVHTFEE 1426  
Qy 1057 VQKNFLSKMKRRRDSGEVLRTAHRVDFDFAKVLGGL-----REQEKRIKCL 1105

Db 1427 ESVEDMKRETKNLSNDRIRHTABRTDAILNRSVSLTQLEFTLKEEIRLEHMKMN 1486  
Qy 1106 ESQ 1108  
Db 1487 DSR 1489  
RESULT 5  
JU0092  
trp protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 17-Nov-2000  
C:Accession: JU0092  
R:Montell, C.; Rubin, G.M.  
Neuron 2, 1313-1323, 1989  
A:Title: Molecular characterization of the Drosophila trp locus: a putative integral membrane protein  
A:Reference number: JU0092; MUID:90180449; PMID:2516726  
A:Accession: JU0092  
A:Molecule type: mRNA  
A:Residues: 1-1275 <MON>  
A:Experimental source: strain Oregon R  
C:Comment: trp protein is expressed predominantly in the rhabdomeric membranes of the photoreceptor  
C:Genetics:  
A:Gene: trp  
A:Cross-references: FlyBase:FBgn0003861  
C:Superfamily: TRP3 protein  
C:Keywords: transmembrane protein  
F:334-354/Domain: transmembrane #status predicted <TM1>  
F:378-401/Domain: transmembrane #status predicted <TM2>  
F:419-436/Domain: transmembrane #status predicted <TM3>  
F:457-471/Domain: transmembrane #status predicted <TM4>  
F:504-527/Domain: transmembrane #status predicted <TM5>  
F:612-630/Domain: transmembrane #status predicted <TM6>  
F:636-661/Domain: transmembrane #status predicted <TM7>  
Query Match 5.4%; Score 326.5; DB 2; Length 1275;  
Best Local Similarity 20.3%; Pred. No. 4.3e-15;  
Matches 178; Conservative 123; Mismatches 264; Indels 313; Gaps 37;  
Qy 305 NITSHOHLTVYDFEGSEELDTVILKALVACKSHSQBPQDYLDLKLAVANDRVDIA 364  
Db 86 NVILLEHIEVGDLALLHAISEYVEAVEELLQWETHKEGQPY-----SWEAVDRS 137  
Qy 365 KSEIFNGDVEWKSCLDEEVVMDALVSNKPEFVRLFVDNGA-----DV 406  
Db 138 KS-FTVDI-----TPLILAAHNNYELIKILLDRGATLPMPHDVKCGDCEVTSQT 188  
Qy 407 ADFLTYGRLO-ELYRSVRSKSLLLFDLQKQBEARLTLAGLGTQQAAREPPAPFAPSLH- 464  
Db 189 TDSLRHSQSRLNAYRALSSALI-----ALSSRDVIL--TAFQLSW 227  
Qy 465 EVSRVLKDFLODACRGFYQDGRPGDGRRAEKGPAKRPQTQKWLDDLNQKSENPRDLFLW 524  
Db 228 ELKRL--QAMESFEAEYTEMR---QMVQDFGTS-----LLDHARTS-----MELE 268  
Qy 525 AVLQNRHEMATYFWAMQOEVAAALACKILKEMSHLETEAARATREAKEYERLALDLF 584  
Db 269 VMLNFNHEPSSHDIWCLGQ-----RQTLER----- 292  
Qy 585 SECYSNSEARAFALLVRRNRKSKTKTCLHLATEADAKAFPAHDGVAQLFTRIWMGDMAAG 644  
Db 293 -----LKAIRYKQKTFVAHPNVQQLAAIWD-----G 321  
Qy 645 TPILRLLAGFLCPALVYNTLITFSBEAPLRTGLEDDQLDLSLDEKSPLYGLQSRVEELV 704  
Db 322 LPGRF-----RKQASQQLMDVVKLG-SPFIYSL-----KYI 352  
Qy 705 EAPRAQGRGRPRAVFLTRWKKFWGAPVTPLGNVVMYFAFLFL----- 748  
Db 353 LAPDSEG-----AKFMRKPFVKIITHSCSYMFFLMLLGAASLRVVOITFELL 399  
Qy 749 -FTVVL--LVDFRPPQ--PSGPEVTLYFWVFTLVLEIR---QGFPTDTHLVKKF 799

Db 400 APPWMLTLEDRKHERGSLPGPIELAIITYIMALIFEELKSLYSDGLFE----- 449

QY 800 TLYVGNWNKCDMAIFLFIIVGVTQR-----MLPS 829

Db 450 --YINDLWNIIVDISNMFVVTWILCRATATWIVHRDLWFRGIDDPYPRHWHPPDFDMLIS 507

QY 830 --AFAGRTVLAMDVFVT-LRLIHIFAIHQKQPKIIVVERMKDVFFFLFSLVMLVA 886

Db 508 EGAFAG-----MVFSYLKLVHIFSINPHGLQVSLGRMIIDIKFFIYTLVLF 559

QY 887 YGVTQALL-----HPHDGRLEW-----IFRRV--LYRP-----YLOIFGQ 920

Db 560 FGCLNQLLWYAELEKKNKYHLHPVADFDQOEKACTIWRFSNLFETSQSFLWASFG 619

QY 921 IPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLVTLVTLNVLNMLLIAMFSY 980

Db 620 VDLVSFDLAGIKS-----FTRFWALLMFGSYSVINIIVLLNMLLIAMNS 663

QY 981 TFQVQGNADMFWKFORYNLIVEYHE-RPALAPPFILLSHLSLTLRRVFKKAEHREHL 1039

Db 664 SYQIISERADTENKFARSQWMSYFDDGTIPPPNLCNMKMLRTGLGRKPSRTKSM 723

QY 1040 ERDL--PDPLDQKVVTWVOKENFLSKMKRRDSEG 1075

Db 724 RKSMEPAQTLDHKVM---KLLVRYIT-AEQRRDDYG 757

RESULT 6

JN0015

trp protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 02-Feb-2001

C:Accession: JN0015

R:Wong, F.; Schaefer, E.L.; Roop, B.C.; LaMendola, J.N.; Johnson-Seaton, D.; Shao, D. Neuron 3, 81-94, 1989

A:title: Proper function of the Drosophila trp gene product during pupal development is A:Reference number: JN0015; PMID:90148782; PMID:2482778

A:Accession: JN0015

A:Molecule type: mRNA

A:Residues: 1-1274 <WON>

C:Comment: This photoreceptor membrane-associated protein is not required for the occur

C:Genetics:

A:Gene: trp

A:Cross-references: FlyBase:Fgn003861

A:Map position: 99C5-6

C:Superfamily: TRPC3 protein

C:Keywords: Glycoprotein; nucleotide binding; P-loop; phosphoprotein; transmembrane pro

F:1257-1263/Region: nucleotide-binding motif A (P-loop)

F:64,70,899/Binding site: carboxylate (Asn) (covalent) #status predicted

F:191,602,883,924/Binding site: phosphate (Ser) (covalent) #status predicted

F:800,1266/Binding site: phosphate (Thr) (covalent) #status predicted

QY 274 VPKVARK-OFKKEFPKSHSWEDIVRTWKILQWITSH-----QHLLTVVDFPEQS 323

Db 48 VKKILEYOGTKF--NINCTDPMNRSAISIENENFDMLVILHEHNEVGDALLHAI 104

QY 324 BELDTVLKALVKACKSHSQEPDYDELKLVADRVDIKSEIFNGDVEMKSCDLBEV 383

Db 105 SERYEAVEBELLQWETNKEGQFY-----SWEAVDRSKS-TFTVDITF----- 147

QY 384 MVDALVSNKPEFVRLFDNGA-----DVADFLYGLRQ-ELYSRVS 424

Db 148 LILAAHNNYELIKILLDRGATLPMPHDVKCGDECVTSTQTTDSLRSQSRIINAYRALSA 207

QY 425 KSLFLDLLQKQEARLTLAGLCTQAREPPAGPPAFSLH-EVSRVLKDFDQACRFFQ 483

Db 208 SSLI-----ALSRDVL--TAPQLSWEKRL--QAMESEFRAEY 244

QY 484 DGRPGDRRAEKGPAPKPTGQKWLLDLNQSENPRDLFLWAVLQNRHEMATYFWANGOE 543

Db 245 EMR---QMYQDEGTS-----LLDHARTS-----MELEVMLNFENHPSHDW 282

QY 544 GVAALAAACKILKEMSHLETEAARATREAKYERIALDLFSECYSNSARAPALLVRN 603

Db 283 -----CLASSET-----LER-- 292

QY 604 RCWSKTTCLHLATEADAKAFFADHGVOAFLTRIWMGDMAAGTPIRLLLGALFLCPALVYTN 663

Db 293 -----LKLAIYKQKTFVAHPNVQQLAAIW-----YDG 321

QY 664 LITFSEAPLRTGLDEDLDLSDTEKSPLYGLQSRVELVAPRAQGRGPRAVFLTR 723

Db 322 LFGFQPEAS-----OQLMDVWKLGC-SFPIYSJL--KYILAPDSEG----- 358

QY 724 WKFWGAPVTVFLGNVVMYFAFLF-----FTYVL--LVDFRPPQG-- 763

Db 359 -AKFMRNPULSSSRTPCPSYMFLLMLLGAASLRVQITFELLAPMMLTWLEDWRKHERGS 417

QY 764 -PSGPEVTLYFWVTLVLEEIR---QGFFTDEDTHLVKKFTLYVGDNNKNCIMVAIFLF 818

Db 418 LFGPIELAITIYIMALIPEELKSLYSDGLFE-----YINDLWNIIVDIYSNMFY 465

QY 819 IVGVTCR-----MLPS--AFAGRTVLAMDPMVT 846

Db 466 VTWILCRATAWIVHRDLWFRGIDPYPRHWHPPDFDMLLSEGAFAG-----MVFS 517

QY 847 -LRLTHIFAIHQKQPKIIVVERMKDVFFFLFSLVMLVANVVTQALL----- 895

Db 518 YLKLWHIFSINPHGLQVSLGRMIIDIKFFIYTLVLFAGCGLNQLLWYAELEKKN 577

QY 896 --HPHDGRLEW-----IFRRV--LYRP-----YLOIFGQIPLDEIDEARVNCSTHPL 939

Db 578 CYHLHPDVADFDDQEKACTIWRFSNLFETSQSFLWASGLVDLVDSFDLAGIKS----- 631

QY 940 LEDSPSCPSLYANWLVILLVTLVTLNVLNMLLIAMFSYTFQVQGNADMFWKFORYN 999

Db 632 -----FTRFWALLMFGSYSVINIIVLLNMLLIAMNSYQIISERADTEWKFARSQ 681

QY 1000 LIVEYHE-RPALAPPFILLSHLSLTLRRVFKKAEHREHLERDL--PDPLDQKVVTWET 1056

Db 682 LMSYFEDGGTIPPPNLCNMKMLRTGLGRKPSRTKSFMRKSMERAQTLDHKVM---K 738

QY 1057 VQKENFLSKMKRRRDEG 1075

Db 739 LLVRYIT-AEQRRDDYG 756

RESULT 7

S40764

hypothetical protein ZK512.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 24-Nov-1999

C:Accession: S40764

R:Hawkins, T.; Ainscough, R. submitted to the EMBL Data Library, February 1993

A:Reference number: S40759

A:Accession: S40764

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1418 <HAW>

A:Cross-references: EMBL:Z22177; NID:g297989; PID:g297992

C:Genetics:

A:Introns: 199/1; 238/1; 290/2; 529/3; 557/3; 588/3; 677/2; 733/3; 846/3; 946/1;

C:Superfamily: Caenorhabditis elegans hypothetical protein ZK512.3

Query Match 4.8%; Score 294; DB 2; Length 1418;

Best Local Similarity 20.2%; Pred. No. 1.2e-12;

Matches 222; Conservative 174; Mismatches 437; Indels 264; Gaps 45;

QY 65 PNLVSVLGEEDFPFAMKSWLRDLVRKGLVKAAQSTGAWILTSAIRVGLARHVGQAVRHS 124

Db 67 PDLIISLISHGNSLSTK--YMSSVENGLKSFILGCTWLISSG-----EYNDPM 113





Db 430 LELIVVMYVIGFVEEVEQEIFAVGMS-----YLRNMWFDLRLNSLY-VSMVC-L 479  
QY 827 LPSAFAGRTVLAMD-----FMVFT-LRLIHFIAHKOL 859  
Db 480 RAFAYIQOATEARDQOMAYIPREKWHDDPQIIAEGLFANAANVFSALKLVHLFSINPHL 539  
QY 860 GKIIIVVMMKDV--FFLFFLSVMLVAYGV--TOALLPHDGRLEW-- 904  
Db 540 GPLQISLGRMVIDIVKFFIYTLVFAFAGLQALLWYFAALEKSKCYLP--GGEADWGS 598  
QY 905 -----IFRRV--LYRP-----YLIQFGQPLDEIDARVNCSTHPLLEDSPSCPSLYAN 952  
Db 599 HGDSCMKRRFGLNLFESSQSLFASFGMVLGDDFELSGIKS-----YTR 642  
QY 953 MLVILLVTLVTLVNTVLLNLLIAMPSYTFQVQGNADMFWKFORNYLIVEHERPA-LA 1011  
Db 643 FWGLLMFGYSVINIVLNLNLLIAMNSYAMIDEHSDTEWKFPARTKYMWSYFEDSATLP 702  
QY 1012 PPFILLSHLSLTLRRVFKKEAEHREHLERDLPDLDQKVVTWETVQKENFLSKMEKRRR 1071  
Db 703 PPFNVLPVKWI-RIFRKS-----KTIDQRSKKRKEQEQF 739  
QY 1072 DSEGEVLRTAHRVDIFIAKVLGLREQ-----EKRIKLESQIN 1110  
Db 740 SEYDNIMR-----SLVMRYVAAHMKFENNPNVSEDDINEVKSEIN 779

RESULT 9  
F88391  
protein R06B10.4 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: F88391  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; PMID:99069613; PMID:9851916  
A>Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: F88391  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-899 <STO>  
A:Cross-references: GB:chr\_III; PIDN:AAB95033.1; PID:g2746879; GSPDB:GN00021; CBSP:R06B1  
C:Gene: R06B10.4  
A:Map position: 3

Query Match 4.1%; Score 247; DB 2; Length 899;  
Best Local Similarity 19.4%; Pred. No. 1.6e-09;  
Matches 166; Conservative 125; Mismatches 312; Indels 252; Gaps 38;  
QY 349 LDELKLVANDRDVDTAKSIFNGDVWKSDDL-----EVMVDALVNKKEPFVRLFVD 401  
Db 32 LREKQFLSCERGDIQSVKRLLAGISTETFNCLDPLGRNALLIAIENIEMIELLID 91  
QY 402 NCADVADFTYKGLQELYSVSRKSLFDLLQKQK--EARLTLAGLGTQOAREPPAGPPA 460  
Db 92 HNIETGDAILYAIGEB--NVRAVEIIVHEKMDKPFDSERQGVETHEHSFTPTDITP 148  
QY 461 FSLHEVSRVLKDFLODACRGFYQDGRPRDRRAEKGPAKRP-----TGQWLL 508  
Db 149 LAAH-----KQYE--CIKFLD-----KKGTVPHPHDVRCSPCEVYAREEDSL 191  
QY 509 DLNQKSENWRDLFLWAVL--QNRHEMATYFWAMQGVGAALAAACKILKEMSHLETEABA 567  
Db 192 RLSRGRINAYRALTGSFLCCLSDARDPILYAFELSW-----LKRSLFIENEFT 240  
QY 568 ARATREAKYERLALDLFSCYNSSEARAFALLVRNRCSKTC-----LHLAT 616  
Db 241 DYEEISQKQKFCVHMLDDQVRGSKLE--VNLNHTTNAHVDVTSANYGNPEKLARLKLA 298  
QY 617 EADAKAFFAHGQVQAFLTRIWMGDMAGTPILRLLAGFLCPALVYTNLITFSEAPLRTG 676

Db 299 QLSQKRFVAHPNCQQLLLDIWY-----EGVESVR-----CTNFIY-KLIFY----- 338  
QY 677 LEDQLDLSLDTKESPLGLQSRVELVEAPRAQGRGPRAVFELL---TRWRKFWCAPVT 733  
Db 339 -----ILGMLSPFLFSL-----VYLLAPHSSMGQFAKKPFI 369  
QY 734 VFLGNVMVYFAFLFPTY-----VLLVD-----FRPPQSGSGPEVTLYFWVFT 777  
Db 370 KFLSHSGSYIFELLILIMASQRMVNDILRTDDVDKETRGP--PTIIECAIFLWVLG 427  
QY 778 LVLEIRQ-----GFTDETHLVKKFTLVXGDMNKNCDMAJFLFIVGTTCRL----- 827  
Db 428 LIWVEIKQLWECGLYN-----YCRNLWNLDIFITNSLYLCTTALRVVAYQVE 475  
QY 828 PSFAFAGR-----TVLAMDPM-----VP-TLRLIHFIAHKLQGP-KII 864  
Db 476 QEALRANSVHIAHLPFRDWDAMDPTLLSECFATANIFSSIKLVHIFTVSPHLGPKIS 535  
QY 865 VVE-----RMMKDV--FFELRFLSVMLVAYGVTTQALLPHDGRLEWIFRRV- 909  
Db 536 LGELEKFKWKKTLKCRWIDIVKFMVVALVLFACGL-----NQLLWYASMR 585  
QY 910 -----LYRPY-----LQIFGQPLDEIDEARVNC-----THPLL 940  
Db 586 QNECNLYEQYKNEKSLSYKYHKLKESCDKDYKSCSIYHTAETFLWALFLVDLTHRLK 645  
QY 941 EDSPSCPSLIYANWLVLLVTLVNTVLLNLLIAMPSYTFQVQGNADMFWKFORNYL 1000  
Db 646 ED-----HFLSEWTKTIFGSCYCCGSIIVLLNMLIAMNSYQISDQDIEMKFARSRL 700  
QY 1001 IVEYHERPA-LAPPFILG--SHLSLTLRRVFKKEAEHREHLERDLPDLDQKVVTWET 1056  
Db 701 FLEYFDDTATLPPPNIVPSPKSIYCHLYLTKLONCTK-----LQPSKQKSM--R 751  
QY 1057 VOKENFLSKMEXRRR 1071  
Db 752 VESKNLAIRQRPKQ 766

RESULT 10  
S44873  
ZC21.2 protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 23-Mar-2001  
C:Accession: S44873  
R:Du, Z.; Waterston, R.  
submitted to the EMBL Data Library, May 1993  
A:Description: Sequence of the C. elegans cosmid ZC21.  
A:Reference number: S44649  
A:Accession: S44873  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-823 <DUZ>  
A:Cross-references: EMBL:L16685; NID:g289729; PIDN:AAA38168.1; PID:g289732  
C:Genetics:  
A:Introns: 47/2; 91/3; 144/1; 215/2; 344/3; 394/3; 440/3; 506/2; 566/3; 756/3  
C:Superfamily: TRP3 protein  
C:Keywords: transmembrane protein

Query Match 3.9%; Score 235.5; DB 2; Length 823;  
Best Local Similarity 20.7%; Pred. No. 9.8e-09;  
Matches 113; Conservative 92; Mismatches 190; Indels 151; Gaps 20;  
QY 549 LAACKILKEMSHLETEABAARAT---REAKYERLALDLFSECYNSSEARAFALLVRNR- 604  
Db 260 LSAPKLSLDLQALAPEHEHEFKETYLQLSQCKQYSCDLLSQCRSEE--VIAILNKDGNV 317  
QY 605 -----CWS-----KTTCLHLATEADAKAFPAHDGVQAFLTRIWMGDMAGTPILRLGA-- 653  
Db 318 NDDNIDVWASKLSRLKLAIKYEQAFVSPHPCQLLTISIWY-----EGIPYQRSSTWA 373  
QY 654 --FLCPALVYTNLITFSEAPLRTGLELDLSDLTESKPLYGL-----QSRVEELVE 705



Db 426 LLILWIIGMIWSDIKRLWYEGLED-----FLEESRNQLSFVNLSYLATFALKVVA 476  
QY 829 -----SAFEAGRTVLAMDPMVFT-----LRLIHFAIHKQLGPKLIIVERMM 870  
Db 477 HNKFDHFAADKOWDAFHP--TLVAEGLFAFANVLSYLRFLFMFTYSSILGLPQISMGQML 534  
QY 871 KDV--FFFLFSLVWLVAVGVTTQALLHPHGDGRLEWIFRRVLYRYPYLOIF--GOIPLDRI 926  
Db 535 QDFGKELGFLVLFVFTIGLT-----QYDKGYTSKEQK 569  
QY 927 D-----EARVNCSTHPLLEDSPSCPSLYANWLV----- 956  
Db 570 DCVGIFCEQSQNDTHSF1---GTCFALF--WYIFSLAHVAIFVTRFSYGEELQSFVGA 623  
QY 957 LLLVTFLLVTVNLLMNLIIAMFSYFOVVQGNADMFWKFORYNLIVEY-HERPALAPPF- 1014  
Db 624 VVGTVNVVVVIVLTLLVAMLHKSPQLIANHEDKEWFAKAKLMLSYFDDKCTLPFPFN 683  
QY 1015 -----ILLSHLSLTLRRVFKKEAEHKEHLE--RDLPPDQKVVTVWTVQK--- 1059  
Db 684 IIPSPKTCIMYMISSLSKWICSHTSKGVKRONSLKEWRNLKQKD-----ENYQVMCC 737  
QY 1060 --ENFLSKMKERRRDSGEVLRTAHRVDFIAKYLGGLRE 1097  
Db 738 LVHRYLTSMRQKMQSTQDATVENNELRQDLSKFRNEIRD 777  
RESULT 13  
I38361  
TRPC1 protein - human  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 04-Sep-1998  
R:Res, P.D.; Chevessich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.  
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995  
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.  
A:Reference number: I38361; MUID:96003837; PMID:7568191  
A:Accession: I38361  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-810 <RES>  
A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787  
C:Superfamily: TRPC3 protein

Query Match 2.9%; Score 176.5; DB 2; Length 810;  
Best Local Similarity 18.1%; Pred. No. 0.00019;  
Matches 116; Conservative 106; Mismatches 215; Indels 203; Gaps 27;  
QY 555 LKEMSHLETE-----AEAARATREAKYERLALDLFSECYSNSPARAF----- 596  
Db 261 LKELSLIVEFRNDYELAR-----QCKMFADLLAQARNSRELVILNHTSSDEPLDKR 315  
QY 597 ALLVRRNCWKTCTLHLATEADAKFAHGDVQAFTRIMWGDMAA--GTPILRLLGAF 654  
Db 316 GLLEER---MNLRLKLAIKVNOKEFVSQSNQQLFNTWFGMSGYRRKPTCKKIMTV 371  
QY 655 LCPALVYTNLITPSEEAPLTGLEDLQDLSLDTKSPLYGLOSRYVEELVEAPRAQDGRG 714  
Db 372 LTVGIFW-----PVLSLCYLI-----APKQ----- 392  
QY 715 PRAVLLTRWRKPGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPPQSGS-----EV 769  
Db 393 -----FGRILHTPFMKFIHGASYFTFLLLNLSLV-VNEDKNTMGALERIDY 442  
QY 770 TLVFWVFTLVLEIROGFFTD-EDTHLVKKFTLYVGDNNKNCMDVAIFLIVGTCRMLP 828  
Db 443 LLILWIIGMIWSDIKRLWYEGLED-----FLEESRNQLSFVNLSYLATFALKVVA 493  
QY 829 -----SAFEAGRTVLAMDPMVFT-----LRLIHFAIHKQLGPKLIIVERMM 870  
Db 494 HNKFDHFAADKOWDAFHP--TLVAEGLFAFANVLSYLRFLFMFTYSSILGLPQISMGQML 551

QY 871 KDV--FFFLFSLVWLVAVGVTTQALLHPHGDGRLEWIFRRVLYRYPYLOIF--GOIPLDRI 926  
Db 552 QDFGKELGFLVLFVFTIGLT-----QYDKGYTSKEQK 586  
QY 927 D-----EARVNCSTHPLLEDSPSCPSLYANWLV----- 956  
Db 587 DCVGIFCEQSQNDTHSF1---GTCFALF--WYIFSLAHVAIFVTRFSYGEELQSFVGA 640  
QY 957 LLLVTFLLVTVNLLMNLIIAMFSYFOVVQGNADMFWKFORYNLIVEY-HERPALAPPF- 1014  
Db 641 VVGTVNVVVVIVLTLLVAMLHKSPQLIANHEDKEWFAKAKLMLSYFDDKCTLPFPFN 700  
QY 1015 -----ILLSHLSLTLRRVFKKEAEHKEHLE--RDLPPDQKVVTVWTVQK--- 1059  
Db 701 IIPSPKTCIMYMISSLSKWICSHTSKGVKRONSLKEWRNLKQKD-----ENYQVMCC 754  
QY 1060 --ENFLSKMKERRRDSGEVLRTAHRVDFIAKYLGGLRE 1097  
Db 755 LVHRYLTSMRQKMQSTQDATVENNELRQDLSKFRNEIRD 794  
RESULT 14  
T34472  
Hypothetical protein W03B1.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T34472  
R:Miller, N.; Bradshaw, H.; Wu, X.; Gattung, S.  
submitted to the EMBL Data Library, June 1998  
A:Description: The sequence of C. elegans cosmid W03B1.  
A:Reference number: Z21532  
A:Accession: T34472  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-823 <MIL>  
A:Cross-references: EMBL:U58753; PIDN:AAC24437.1; GSPDB:GN00022; CESP:W03B1.2  
A:Experimental source: strain Bristol N2; clone W03B1  
C:Genetics:  
A:Gene: CESP:W03B1.2  
A:Map position: 4  
A:Introns: 70/3; 102/1; 137/2; 187/2; 265/3; 293/3; 357/3; 489/3; 516/1; 604/2; 628/2  
Query Match 2.7%; Score 165; DB 2; Length 823;  
Best Local Similarity 22.9%; Pred. No. 0.0014;  
Matches 104; Conservative 64; Mismatches 175; Indels 112; Gaps 21;  
QY 771 LYFWFTLV-----LBEIRQ---GPTDEDTHLVKKFTLYVGDNNKNCMDVAIFLIVGV 822  
Db 406 LAFWRIVLVVPLLTLEAARLLIFAFVIEKKSSDKNF-----WSGA-----WVLIPI 452  
QY 823 TCRMLPSAFEAGRTVLAMDPMVFTLRLIHFHAIKOLGPKLIIVERMKDV-FFFLFLLS 881  
Db 453 TLELLYCALFATAT-----VSTLRFFHSI---QSLGFFIHLFKOMKMTVGMFILFCT 502  
QY 882 VMLVAVGVTTQALLHPHGDGR-----EWIFRRVLYRYPYLOIFGOIPLDRIEAVR---N 932  
Db 503 FWFVL-----AVIHVVISRTLLATSNISFLYTVTFQKFEIAGEVQ-----DEDRI GILLN 552  
QY 933 CSTHPLLED-----SPSCPSLYANWLVLLVTFLLVTVNLLMNLIIAMFSYFOVV 985  
Db 553 CSEYNKTMVEFFDMBYAEASC--LFRSTIMPVFWFTYIFVTGILLVNLITAQLTKEYENE 610  
QY 986 QGNADMFWKFORYNLIVEYHERPALAPPFILL----- 1017  
Db 611 SKNSAYKYLKYEQTUKIESKLYLPPPSLFFVULRFWYSCFFKIVIFTWLTSGCCK 670  
QY 1018 ---SHLSLTLRRVFKKEAEHKEHLELDPLDQKVVTVWTVQKFNLSKME-----K 1068  
Db 671 CSSTAISLYWNRIVRIVEGYPGAVRQTDNEIDTKVAEFLRKPDPNALEKULVNNYD 730  
QY 1069 RRRDSEGEVLRTAHRV-DFIAKYLGGLREQKRIKCLSQINYSVLVSVSVADVLAQGG 1127  
Db 731 KOVDDE-EALKKLGKEIKKFLAKEIG--ERERASQNSLENHPRSGVLDPKKKHRLS--- 784

Search completed: September 14, 2004, 00:06:41  
Job time : 34 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 14, 2004, 00:01:53 ; Search time 71 Seconds  
(without alignments)

5177.165 Million cell updates/sec

Title: US-10-026-188-8

Perfect score: 6093

Sequence: 1 MQDVQGPFGSGDAEDRRRE.....HRGGLDGEQPGAGPPSDT 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6093	100.0	1165	4 Q9NZQ8	Q9nzq8 homo sapien
2	6039	99.1	1159	4 Q9NY34	Q9ny34 homo sapien
3	5088.5	83.5	1158	11 Q9JUH7	Q9jyh7 mus musculus
4	5036.5	82.7	1148	11 Q9EPM4	Q9epm4 mus musculus
5	5026.5	82.5	1148	11 Q9NFM9	Q9nfm9 mus musculus
6	4981.5	81.8	1116	11 Q9EPM3	Q9epm3 mus musculus
7	4465.5	73.3	1030	11 Q8BS44	Q8bs44 mus musculus
8	4354.5	71.5	1000	11 Q7TPL4	Q7tpl4 mus musculus
9	2448.5	40.2	1214	4 Q8TD43	Q8td43 homo sapien
10	2399.5	39.4	1213	11 Q7TN37	Q7tn37 mus musculus
11	2184.5	35.9	1040	4 Q96L84	Q96l84 homo sapien
12	2164	35.5	1016	4 Q9XNV1	Q9nxv1 homo sapien
13	2098	34.4	1069	4 Q725D9	Q725d9 homo sapien
14	2069	34.0	945	11 Q8BLM7	Q8blm7 mus musculus
15	2021	33.2	1507	11 Q91YD4	Q91yd4 mus musculus
16	1722	28.3	793	11 Q80Y94	Q80y94 mus musculus

## ALIGNMENTS

### RESULT 1

Q9NZQ8 PRELIMINARY; PRT; 1165 AA.

AC Q9NZQ8; DT 01-OCT-2000 (TREMELrel. 15, Created)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DE MTRI.  
DE MTRI.  
GN MTRI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20076317; PubMed=10607831;  
RA Prawitt D., Enklaar T., Klemm G., Gaertner B., Spangenberg C., Winterpacht A., Higgins M., Pelletier J., Zabel B.;  
RT Identification and characterization of MTRI, a novel gene with homology to melastatin (MLSN1) and the trp gene family located in the BWS-WT2 critical region on chromosome 11p15.5 and showing allele-specific expression.";  
RL Hum. Mol. Genet. 9:203-216(2000).  
DR EMBL; AF177473; AAF26288.1; -.  
DR Genew; HGNC:14323; TRPMS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPR002111; Cat channel\_TrpL.  
DR InterPro; IPR005821; Ion\_trans.  
DR Pfam; PF00520; ion\_trans; 1.  
KW Ionic channel; Transmembrane.  
SQ SEQUENCE 1165 AA; 131450 MW; C4AD5BAA866BE73B CRC64;

Query Match 100.0%; Score 6093; DB 4; Length 1165;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQDVQGPFGSGDAEDRRRELGLHRGEVNFVFGSGKKRGKGFVRVPSGVAPSLFDLLAEW 60

Db 1 MQDVQGPFGSGDAEDRRRELGLHRGEVNFVFGSGKKRGKGFVRVPSGVAPSLFDLLAEW 60

Q8r4d5 mus musculus  
Q7t0w9 xenopus lae  
Q8r455 ratus norv  
Q72zw7 homo sapien  
Q8tdx8 homo sapien  
Q8tac3 homo sapien  
Q86ul0 homo sapien  
Q86wk3 homo sapien  
Q86z00 homo sapien  
Q86wk2 homo sapien  
Q86sh6 homo sapien  
Q86wk1 homo sapien  
Q86wk4 homo sapien  
Q86z01 homo sapien  
Q86sh0 homo sapien  
Q86yz9 homo sapien  
Q724n1 homo sapien  
Q75560 homo sapien  
Q724n5 homo sapien  
Q724n2 homo sapien  
Q724n4 homo sapien  
Q925b2 mus musculus  
Q923j1 mus musculus  
Q91lq1 mus musculus  
Q9bxb2 homo sapien  
Q96ct4 homo sapien  
Q9b84 homo sapien  
Q8cir4 mus musculus  
Q80yb3 mus musculus



QY 487 PGDRRAEKGPAKPTCKQKWLDDNOKSENPRDLFLWAVLQNRHEMATYFWAMQSGVA 546  
 DB 481 PGDRRAEKGPAKPTCKQKWLDDNOKSENPRDLFLWAVLQNRHEMATYFWAMQSGVA 540  
 QY 547 AALAAACKILKEMSHLETEAARATREAKYERIALDLDFSECYSNSEARAFALLVRRNCW 606  
 DB 541 AALAAACKILKEMSHLETEAARATREAKYERIALDLDFSECYSNSEARAFALLVRRNCW 600  
 QY 607 SKTTCHLATEADAKAFFAHGQVAFTRIWWGDMAGTPTILRLGAFGLCPALVYTNLIT 666  
 DB 601 SKTTCHLATEADAKAFFAHGQVAFTRIWWGDMAGTPTILRLGAFGLCPALVYTNLIT 660  
 QY 667 FSEEAPELRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQDGRPRAVFLTLNRWK 726  
 DB 661 FSEEAPELRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQDGRPRAVFLTLNRWK 720  
 QY 727 FWGAPVTVFLGNVVMYFAFLFETLYVLLVDFRPPQSPGPEVTLYFWVFTLVLEIRQG 786  
 DB 721 FWGAPVTVFLGNVVMYFAFLFETLYVLLVDFRPPQSPGPEVTLYFWVFTLVLEIRQG 780  
 QY 787 FFTDETHLVKFTLVYGVGNWKNKCDMVAIFLFIYGVVTCRMLPSAFEAGRTVLAMDWFVFT 846  
 DB 781 FFTDETHLVKFTLVYGVGNWKNKCDMVAIFLFIYGVVTCRMLPSAFEAGRTVLAMDWFVFT 840  
 QY 847 LRLIHFAIKHQLGPKIIVVERMMKDVFFFLFSLVNLVAYGVTTQALLHPHGDRLWEIF 906  
 DB 841 LRLIHFAIKHQLGPKIIVVERMMKDVFFFLFSLVNLVAYGVTTQALLHPHGDRLWEIF 900  
 QY 907 RRVLYRPYLIQFQIPLDEIDEARVNCSTHPLLEDSPSPSYANWLVILLVTFLLVT 966  
 DB 901 RRVLYRPYLIQFQIPLDEIDEARVNCSTHPLLEDSPSPSYANWLVILLVTFLLVT 960  
 QY 967 NVLLNMLLIAMFSYTFQVVGQADMFVKFORYNLIVEYHERPALAPPEFILLSHLSLTLRR 1026  
 DB 961 NVLLNMLLIAMFSYTFQVVGQADMFVKFORYNLIVEYHERPALAPPEFILLSHLSLTLRR 1020  
 QY 1027 VPKKEAHEKREHLERDLDPDQKVVTWETVQKENFLSKMEKRRRDESEVLKRTAHRVD 1086  
 DB 1021 VPKKEAHEKREHLERDLDPDQKVVTWETVQKENFLSKMEKRRRDESEVLKRTAHRVD 1080  
 QY 1087 FIATYVGLGUREQKRIKCLSEQINYSVLVSSVADYLAQGGPRSSQHGEGSOLVAADH 1146  
 DB 1081 FIATYVGLGUREQKRIKCLSEQINYSVLVSSVADYLAQGGPRSSQHGEGSOLVAADH 1140  
 QY 1147 RGGLDGWEQAGQPPSDT 1165  
 DB 1141 RGGLDGWEQAGQPPSDT 1159

RESULT 3  
 Q9JUH7  
 ID Q9JUH7 PRELIMINARY; PRT; 1158 AA.  
 AC 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE MLSN1-and TRP-related protein 1 (MTR1) (Transient receptor potential  
 DE cation channel subfamily M member 5).  
 GN TRPM5 OR LTRPC5 OR MTR1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP PubMed=10907850;  
 RA Yatsuki H., Watanabe H., Hattori M., Joh K., Soejima H., Komoda H.,  
 RA Xin Z., Zhu X., Higashimoto K., Nishimura M., Kuratomi S., Sasaki H.,  
 RA Sakaki Y., Mukai T.;  
 RT "Sequence-based structural features between Kv1qt1 and Tapal on mouse  
 RT chromosome 7F4/F5 corresponding to the Beckwith-Wiedemann syndrome  
 RT region on human 11p15.5: long-stretches of unusually well conserved

intronic sequences of Kv1qt1 between mouse and human.";  
 RL DNA Res. 7:195-206(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20366135; PubMed=10903843;  
 RA Enklaar T., Esswein M., Oswald M., Hilbert K., Winterpacht A.,  
 RA Higgins M., Zabel B., Prawitt D.;  
 RT "Wrl1, a Novel Biallelically Expressed Gene in the Center of the Mouse  
 RT Distal Chromosome 7 Imprinting Cluster, is a Member of the Trp Gene  
 RT Family.";  
 RL Genomics 67:179-187(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=129/SvxC57BL; TISSUE=lung;  
 RX MEDLINE=22726392; PubMed=12842017;  
 RA Hofmann T., Chubakov V., Gudermann T., Montell C.;  
 RT "TRPM5 is a Voltage-Modulated and Ca(2+)-Activated Monovalent  
 RT Selective Cation Channel.";  
 RL Curr. Biol. 13:1153-1158(2003).  
 DR EMBL; AB039952; BAA96877.1; -;  
 DR EMBL; AF228681; AAF98120.1; -;  
 DR EMBL; AY280364; AAF44476.1; -;  
 DR MGD; MGI:1861718; Trpm5.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005261; F:cation channel activity; IEA.  
 DR GO; GO:0006812; P:cation transport; IEA.  
 DR InterPro; IPR002111; Cat\_channel\_trpL.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR Pfam; PF00520; ion\_trans; 1.  
 KW Ionic channel; Receptor; Transmembrane.  
 SQ SEQUENCE 1158 AA; 130843 MW; FOA5237EC67867CE CRC64;

Query Match 83.5%; Score 5088.5; DB 11; Length 1158;  
 Best Local Similarity 84.1%; Pred. No. 0;  
 Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY 1 MDQVQPRPGSGDADREELGLHGEVNFVFGSGKKRGKRVFVPSVAPSVLFLLLAEW 60  
 DB 1 MQTTQSSCGSPDIEDGWEPLCTGGEINFGSGKKRGKRVFVPSVAPSVLFLLLTEW 60  
 QY 61 HLPAPNLVSVLVEGEQPFAMKSWLRDLVRKGLVKAQSTGAMILTSALRVGLARHVQAV 120  
 DB 61 HLPAPNLVSVLVEGERPLAMKSWLRDLVRKGLVKAQSTGAMILTSALRVGLARHVQAV 120  
 QY 121 RDHSLASTSTKRVVAVGVASLGRVLRRLILB--EAQEDFPVHYPEDDGGSGQPLCSLDS 178  
 DB 121 RDHSLASTSTKLRVVAIGNASLDRLHRLQDLDGVHQKEDTRIHYFADEGNIQGPLCLDS 180  
 QY 179 NLSHFILVEPGPGKGG-DGLTELRLRLKHLHSEQAGYGGTSGIETPVLCLLVNGDPNTL 237  
 DB 181 NLSHFILVESGALSGNDGLTELQLSLEKHSQQRTGYGTGTCIPIVCLLVNGDPNTL 240  
 QY 238 ERISRAVEQAAPWLLVVGSGGIADVLAALVNQPHLLVPKVAEKQKFKPPSKHFSWEDIV 297  
 DB 241 ERISRAVEQAAPWLLVLAGSGGIADVLAALVSPHLLVPQVAEKQKFKPPSKHFSWEDIV 300  
 QY 298 RWTLLQNTSHOHLITVYDFEQQSESLDITVILKALVKACKSHQSQBQDYLDLKLAVA 357  
 DB 301 HMTLLQNTIAHPHLLTYDFEQQSESLDITVILKALVKACKSHQSQBQDYLDLKLAVA 360  
 QY 358 WDRVDIAKSEIFNGDVWKSQDLERVMYDALVSNKPEFVLFVDNGADVADFLTYGRLOE 417  
 DB 361 WDRVDIAKSEIFNGDVWKSQDLERVMYDALVSNKPEFVLFVDNGADVADFLTYGRLOE 420  
 QY 418 LYRSVSRKSLPDLQKQEEARLTLAGLGTQAREPPAGPPAFSLHVSRLVKDFLODA 477  
 DB 421 LYHSVSPKSLPDLQKQEEARLTLAGLGTQAREPPAGPPAFSLHVSRLVKDFLODA 480  
 QY 478 CRGFYQDGRDPRRAEKGPAKPTGQKWLDDNOKSENPRDLFLWAVLQNRHEMATYF 537  
 DB 481 CRGFYQDGRDPRRAEKGPAKPTGQKWLDDNOKSENPRDLFLWAVLQNRHEMATYF 536  
 QY 538 WAMQGEVAAALAAACKILKEMSHLETEAARATREAKYERIALDLDFSECYSNSEARAF 597

Db 537 WAMGREGVAAALAAACKIIKEMSHLEKEAEVARTWREAKYEQALDLDFSECYNSSEDRAPA 596  
Qy 598 LLVRNRCWKTTCCLHLATEADAKAFADHGVQAFTRIWWGDMAGTPIILRLGAFCLP 657  
Db 597 LLVRNHSWSRTTCLHLATEADAKAFADHGVQAFTRIWWGDMATGPIILRLGAFCTP 656  
Qy 658 ALVVTNLITSEBAPRTGLEDLQDLSDTEKSPLYGLQSRVBELEAPRAQDGRGPA 717  
Db 657 ALIYTNLISFSEDAPQMDLEDLQEPDSDLMEKSFCLSRGQLEKLEAPAPGDLGPA 716  
Qy 718 VFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDPRPPQSGSPBVTLYFWVFT 777  
Db 717 AFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDPRPPQSGSPBVTLYFWVFT 776  
Qy 778 LVLBEIRQGFTEDETHLVKFTLYVGDNNKCDMVAIFLIVGTCMLPSAFEAGRTV 837  
Db 777 LVLBEIRQGFTEDETHLVKFTLYVEDNNKCDMVAIFLIVGTCMRVPSFEAGRTV 836  
Qy 838 LAMDFMVFTLRLIHI FAHKQLGPKIIIVVERMKDVFFFLFSLVWLVAVGTTQALLHP 897  
Db 837 LAIDFMVFTLRLIHI FAHKQLGPKIIIVVERMKDVFFFLFSLVWLVAVGTTQALLHP 896  
Qy 898 HDGRLEWIFRRVLYRPYLOIFQIPLDIDIDEARVNCSTHPLLEDSPSCPSLYANLVIL 957  
Db 897 HDGRLEWIFRRVLYRPYLOIFQIPLDIDIDEARVNCSTHPLLEDSPSCPSLYANLVIL 956  
Qy 958 LLVTFLLVTNVLNLLIAMFSTYFQVQGNADMPKQRYNLIVYHERPALAPFFILL 1017  
Db 957 LLVTFLLVTNVLNLLIAMFSTYFQVQGNADMPKQRYNLIVYHERPALAPFFILL 1016  
Qy 1018 SHLSITLRRVFKAEHREHLERDLPDQKVVTWETVQKENFLSKMEKRRRDEGEV 1077  
Db 1017 SHLSVLKQVRKEAQHREHLERDLPDQKVVTWETVQKENFLSKMEKRRRDEGEV 1076  
Qy 1078 LRKTAHRVDFIAKYLGLRBEKRIKLESQINYSVLSVADVIAOGGPRSSOHGCE 1137  
Db 1077 LRKTAHRVDFIAKYLGLRBEKRIKLESQINYSVLSVADVIAOGGPRSSOHGCE 1136  
Qy 1138 GSOLVAADHRGGLDQWQEGAGQPPSDT 1165  
Db 1137 RSQPASARDREYLE-----SGLPSPSDT 1158  
RESULT 4  
Q9EPM4 PRELIMINARY; PRT; 1148 AA.  
ID Q9EPM4  
AC Q9EPM4;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE LTRC5 protein.  
GN TRPM5 OR LTRPC5.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129 SV;  
RX MEDLINE=20377495; PubMed=10915772;  
RA Paulsen M., El-Maarri O., Engemann S., Stroedicke M., Franck O.,  
RA Davies K., Reinhardt R., Reik W., Walter J.;  
RT "Sequence conservation and variability of imprinting in the Beckwith-  
RT Wiedemann syndrome gene cluster in human and mouse.";  
RL Hum. Mol. Genet. 9:1829-1841(2000).  
DR EMBL; AJ251835; CAC19456.1; -.  
DR MGD; MGI:1861718; Trpm5.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005261; F:cation channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR InterPro; IPR002111; Cat\_channel\_TrpL.  
DR InterPro; IPR005821; Ion\_Trans.

DR Pfam; PF00520; ion\_trans; 1.  
KW Ionic channel; Transmembrane.  
SQ SEQUENCE 1148 AA; 129630 MW; 947AF5B9CFDCA127 CRC64;  
Query Match 82.7%; Score 5036.5; DB 11; Length 1148;  
Best Local Similarity 85.5%; Pred. No. 0;  
Matches 966; Conservative 63; Mismatches 94; Indels 7; Gaps 3;  
Qy 1 MQDVQSGRPGSGDAEDRELGLHREVNFGGSGKKGKGVPSGVAPSVFLPILLAEW 60  
Db 1 MQTQSSCPGSPDTEDEGWEPILCRGEINFGGSGKKGKGVPSGVAPSVFLPILLAEW 60  
Qy 61 HLPAPNLVSLVGEQPFAMKSWLRDLRWGLVKAAGTGAWILTSALRVGLARHVQAV 120  
Db 61 HLPAPNLVSLVGEERFLAMKSWLRDLRWGLVKAAGTGAWILTSALRVGLARHVQAV 120  
Qy 121 RDHSLASTSTKRVVAVGMASLGRVLRHRRILE--EAQEDFPVHYPEDDGGSGQSLCLSDS 178  
Db 121 RDHSLASTSTKRVVAVGMASLGRVLRHRRILE--EAQEDFPVHYPEDDGGSGQSLCLSDS 180  
Qy 179 NLSHFILVEPPGPGK-DGLTEURLRLEKHSERAGYGGTGSIEIPVLCLLVNGDNTL 237  
Db 181 NLSHFILVESGALSGNDGLTELQLSLEKHSIQORTGYGGTSCIQIPVLCLLVNGDNTL 240  
Qy 238 ERISRAVEQAAPWLLIYSGGIAADVLAALYNOPHLVPAEAKQKPKPSKHSWEIV 297  
Db 241 ERISRAVEQAAPWLLIYSGGIAADVLAALVSQPHLLVPQVAEKQFREKFPSECSWEIV 300  
Qy 298 RWTLLQNIITSHOHLITVYDFEQSGSEBELDTVILKALVKACKSHSQEPQDYLDELKAVA 357  
Db 301 HWTLLQNIIAHPHLLITVYDFEQSGSEBELDTVILKALVKACKSHSQEAQDYLDELKAVA 360  
Qy 358 WDRVDIAKSEITFNGDVWEKSCDLBEVMDALVSNKPEFVRLFVNGADVAADFLTYGRLOE 417  
Db 361 WDRVDIAKSEITFNGDVWEKSCDLBEVMTDALVSNKPDFVRLFVDSGADMAEFLTYGRLOE 420  
Qy 418 LYRSVRSKSLFDLLQKQEBEARLTLAGLGTQQAAREPPAGPAPSLHESVRSVLKDFLODA 477  
Db 421 LYHSVSPSKLFFELLQKHEEGRUTLAGLGAQAARELPGLPAPSLHESVRSVLKDFLHDA 480  
Qy 478 CRGFYQDGRPGDRRAEKGPAKRPTGQKLLDLNOKSENPRDILFLWALVQNRHMAITYF 537  
Db 481 CRGFYQDQ---RRMEERGPPKRPAGQKWLPLDSKSDPWRDLFLWALVQNRHMAITYF 536  
Qy 538 WAMQEGVAAALAAACKIILKEMSHLETEAABARAAREAKYERIALDLFSECYSNSBARAPA 597  
Db 537 WAMGREGVAAALAAACKIILKEMSHLEKEAEVARTWREAKYEQALDLFSECYNSSEDRAPA 596  
Qy 598 LLVRNRCWKTTCCLHLATEADAKAFADHGVQAFTRIWWGDMAGTPIILRLGAFCLP 657  
Db 597 LLVRNHSWSRTTCLHLATEADAKAFADHGVQAFTRIWWGDMATGPIILRLGAFCTP 656  
Qy 658 ALVVTNLITSEBAPRTGLEDLQDLSDTEKSPLYGLQSRVBELEAPRAQDGRGPA 717  
Db 657 ALIYTNLISFSEDAPQMDLEDLQEPDSDLMEKSFCLSRGQLEKLEAPAPGDLGPA 716  
Qy 718 VFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDPRPPQSGSPBVTLYFWVFT 777  
Db 717 AFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDPRPPQSGSPBVTLYFWVFT 776  
Qy 778 LVLBEIRQGFTEDETHLVKFTLYVGDNNKCDMVAIFLIVGTCMLPSAFEAGRTV 837  
Db 777 LVLBEIRQGFTEDETHLVKFTLYVEDNNKCDMVAIFLIVGTCMRVPSFEAGRTV 836  
Qy 838 LAMDFMVFTLRLIHI FAHKQLGPKIIIVVERMKDVFFFLFSLVWLVAVGTTQALLHP 897  
Db 837 LAIDFMVFTLRLIHI FAHKQLGPKIIIVVERMKDVFFFLFSLVWLVAVGTTQALLHP 896  
Qy 898 HDGRLEWIFRRVLYRPYLOIFQIPLDIDIDEARVNCSTHPLLEDSPSCPSLYANLVIL 957  
Db 897 HDGRLEWIFRRVLYRPYLOIFQIPLDIDIDEARVNCSTHPLLEDSPSCPSLYANLVIL 956  
Qy 958 LLVTFLLVTNVLNLLIAMFSTYFQVQGNADMPKQRYNLIVYHERPALAPFFILL 1017  
Db 957 LLVTFLLVTNVLNLLIAMFSTYFQVQGNADMPKQRYNLIVYHERPALAPFFILL 1016





OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129 SV;  
 RX MEDLINE=20377495; PubMed=10915772;  
 RA Paulsen M., El-Waari O., Engemann S., Stroedicke M., Franck O.,  
 Davies K., Reinhardt R., Reik W., Walter J.;  
 RA "Sequence conservation and variability of imprinting in the Beckwith-  
 RT Wiedemann syndrome gene cluster in human and mouse.";  
 RL Hum. Mol. Genet. 9:1829-1841(2000).  
 DR EMBL; AJ251835; CAC19457.1; -.  
 DR MGD; MGI:1861718; Trpm5.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0005261; P: cation channel activity; IEA.  
 DR GO; GO:0006812; P: cation transport; IEA.  
 DR InterPro; IPR002111; Cat\_channel\_TripL.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR KW Ionic channel; Transmembrane.  
 SQ SEQUENCE 1116 AA; 126608 MW; 32DFFABCF2835E48 CRC64;  
 Query Match 81.8%; Score 4981.5; DB 11; Length 1116;  
 Best Local Similarity 85.8%; Pred. No. 0;  
 Matches 956; Conservative 60; Mismatches 91; Indels 7; Gaps 3;  
 QY 1 MQDVQPRPGSGDAEDRELGLHGEVNFSGSKGKGFVVPVSGVAPSVLFDLLAEW 60  
 DB 1 MQTTQSSCGSPPTDGEWELRCRGEINFGSGKKGKGFVVPVSSVAPSVLFDLLAEW 60  
 QY 61 HLPAPNLVSLVGEQPPAMKSLRDLVRLKGLVKAQAQSTGAWILTSALRVGLARHVQAV 120  
 DB 61 HLPAPNLVSLVGEERPLAMKSLRDLVRLKGLVKAQAQSTGAWILTSALRVGLARHVQAV 120  
 QY 121 RDHSLASTSTKRVVAVGMSLRVLRHRIIE--EAQEDPVHPEDDGGSGQPLCSLDS 178  
 DB 121 RDHSLASTSTKRVVAVGMSLRVLRHRIIE--EAQEDPVHPEDDGGSGQPLCSLDS 178  
 QY 179 NLSHFILVPEPPGKG-DGLTELRLRLKHHISEQAGVGGTGTSEIPVLCILVNGDPNLT 237  
 DB 181 NLSHFILVESGALSGNDGLTELQSLSEKHISQORTGYGGTSCIQIPVLCILVNGDPNLT 240  
 QY 238 ERISRAVEQAAPWILLVGGSGIADVIAALVNPQPHLLVPKVAEKQFKKFPKSHFSEWIDV 297  
 DB 241 ERISRAVEQAAPWILLVGGSGIADVIAALVNPQPHLLVPKVAEKQFKKFPKSHFSEWIDV 297  
 QY 298 RWTLLQNTSHOHLTVYDFEQSGSELDITVILKALVKAACKSHSQEPQDYLDLKLAVA 357  
 DB 301 HWTLLQNTSHOHLTVYDFEQSGSELDITVILKALVKAACKSHSQEPQDYLDLKLAVA 357  
 QY 358 WDRVDIAKSEIFNGDVWKSQDLERVMVDALVSNKPEFVRLVFDNGADVADFLTYGRLOE 417  
 DB 361 WDRVDIAKSEIFNGDVWKSQDLERVMVDALVSNKPEFVRLVFDNGADVADFLTYGRLOE 417  
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 DB 481 CRGFVQDGRPGRRRAEKGPAKPTGQKWLIDLKQSENPRDILFLWVQLQNHEMATYF 537  
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 DB 537 WAMQGVAAALAAACKILKMSHLTEAARATREAKYERLALDLFSECVSNSEARAF 596  
 QY 598 LLVRNRCKSWTKTCLHATEADAKAFFAGHDGVOAFLTRIMWGDMAAGTPIRLLAGAFLCP 657  
 DB 597 LLVRNRCKSWTKTCLHATEADAKAFFAGHDGVOAFLTRIMWGDMAAGTPIRLLAGAFLCP 656  
 QY 658 ALVYTNLTFFSEAPITRGLELDQLDSLDTSEKSPLYGLOSVEELVEAPRAQGRGPRA 717  
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Db 657 ALVYTNLTFFSEAPITRGLELDQLDSLDTSEKSPLYGLOSVEELVEAPRAQGRGPRA 716  
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 QY 838 LAMDFVFTLRLHFAIHKOLGPKIIVVERMKDVFELFFLSVWLVAVGTVTQALLHP 897  
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 QY 958 LLVTFLLVTVNLLMNLIIAMFSYTFVQVQGNADFWKFORNLIVEHERPALAPPFTILL 1017  
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 QY 1018 SHLSLTIRRYFKKEAEHREHLERDLDPDLDQKVTVTWETVOKENFLSKMEKRRRDSGEV 1077  
 Db 1017 SHLSLTIRRYFKKEAEHREHLERDLDPDLDQKVTVTWETVOKENFLSKMEKRRRDSGEV 1076  
 QY 1078 LRKTAHRVDFTAKYLGGLRQEKRIKLESQINY 1111  
 Db 1077 LRKTAHRVDLAKYIGGLRQEKRIKLESQSKY 1110  
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 ID QBS44  
 AC QBS44;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE Transient receptor potential cation channel (Fragment).  
 GN TRPM5.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; Tissue=Embryo;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK035197; BAC28976.1; -.  
 DR MGD; MGI:1861718; Trpm5.  
 DR GO; GO:0016020; C: membrane; IEA.  
 DR GO; GO:0005261; P: cation channel activity; IEA.  
 DR GO; GO:0006812; P: cation transport; IEA.  
 DR InterPro; IPR002111; Cat\_channel\_TripL.  
 DR InterPro; IPR005821; Ion\_trans.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR NON\_TER 1  
 FT SEQUENCE 1030 AA; 116983 MW; DDB31B7DF238F402 CRC64;  
 SQ SEQUENCE 1030 AA; 116983 MW; DDB31B7DF238F402 CRC64;  
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 Best Local Similarity 84.4%; Pred. No. 0;  
 Matches 858; Conservative 56; Mismatches 91; Indels 11; Gaps 3;  
 QY 151 LEEAQEDPIHYPADEGNIQGPLCLDSNLSHFLIVPEPPGPKG-DGLTELRLRLKHHIS 209  
 Db 25 LSLAQEDPIHYPADEGNIQGPLCLDSNLSHFLIVPEPPGPKG-DGLTELRLRLKHHIS 84  
 QY 210 EORAGYGGTGTSEIPVLCILVNGDPNLTSEKSPLYGLOSVEELVEAPRAQGRGPRA 269

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OC	Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;	
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RC	STRAIN=129/SvxC57BL; TISSUE=Testis;
RK	MEDLINE=22726392; PubMed=12842017;
RA	Hofmann T., Chubakov V., Gudermann T., Montell C.;
RT	"TRPWS Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
RT	Selective Cation Channel.";
RL	Curr. Biol. 13:1153-1158(2003).
DR	EMBL; AY280365; AAP44477.1; -.
KW	Receptor.
SQ	SEQUENCE 1000 AA; 112459 MW; BB10761017656660 CRC64;
Query Match	71.5%; Score 4354.5; DB 11; Length 1000;
Best Local Similarity	84.4%; Pred. No. 0;
Matches 842; Conservative	53; Mismatches 92; Indels 11; Gaps 4;
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DB	61 HLPAPNLVSLVGEERPLAMKSWLRDLVRKGLVKAAQSTGAWILTSALHVLGLARHVGQAV 120
QY	121 RHSLASTSTKVRVAVGASLGRVLHRRILE--EAQEDFPVHYPEDDGGSGPLCLSDS 178
DB	121 RHSLASTSTKVRVAVGASLDRILHRLDGVHQKEDTPIHPADEGNIQGSLCLPLDS 180
QY	179 NLSHFILVPGPPGKG-DGLTELRLRLKHI SEQRAGYGGTGSIEIPVLCLLVNGDPNTL 237
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QY	298 RWTLLQNTTSHOILLTVYDFQEGSEELDTVILKALVKAKSHSQEPDYLDELKLAVA 357
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QY	358 WDRVDIAKSEIFNGDVEWKSCDLEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLOE 417
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QY	418 LYRSVRSKSLLDILLQKQEEARLTLAGLTQQAAREPPAGPPAFSLHVEVSRVLKQFLODA 477
DB	421 LYHSVSPKSLFELQKQHEEGRLLTLAGLGAQAARELPGLPAFSLHVEVSRVLKQFLHDA 480
QY	478 CRGFYQDGRPGRRRAEKGPAKRGTKQKWLLDNCKSNPARDLFLWALQNRHEWATYF 537
DB	481 CRGFYQDG----RRMEERGPPKRPAGQKWLPLDSRKSEDPRDRLFLWALQNRHEWATYF 536
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QY	598 LLVRRNRCWSKTTCLHLATEADAKAFFAHDGVQAPFLTRIMWGDMAAGTPILRLIGAFTCP 657
DB	597 LLVRRNHSWSRTCLHLATEADAKAFFAHDGVQAPFLTKIMWGDMAATGTPILRLIGAFTCP 656
QY	658 ALVYTNLLTTFSEEAPLRTGLDLDLSDLTEKSPLYGQSRVRELVAPRAQCDGRPA 717
DB	657 ALIYTNLLSFSEDAPOQMDLSDLQEPDSDLMKESFLCSRGQGLEKLTAPRAPGLDGPQA 716
QY	718 VFLLTRMRKFGAPVTFLGNVMVYFAFLFTVYLLVDFRPPPPQSGSEVTTYFWVFT 777
DB	717 AFLLTRMRKFWGAPVTFLGNVMVYFAFLFTVYLLVDFRPPPPQSGSEVTTYFWVFT 776
QY	778 LVLEIRIOGFTDDETHLVKFTLLVYVDNWNKCDMVAIFLFIQVTCRMLPSAFEAGRTV 837

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Db 777 LVLEIRQGFDTEDTHLVKKFTLYVEDNNKCDMAIFLFLVGVTCRMVPSVFEAGRTV 836
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Db 837 LAIDFWFTLRLIHI FAIHKQLGPKIIIVVERMKDVFFFLFSVWLVAIVTQALLHP 896
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Db 957 LLVTFLLVTNVLNLLIAM----FRVLTETGPMSTWF 990

RESULT 9
Q8TD43 PRELIMINARY; PRT; 1214 AA.
AC Q8TD43;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE cation channel TRPM4B (transient receptor potential cation channel
DE subfamily M member 4 splice variant B) (transient receptor potential
DE ion channel melastatin subgroup member 4 protein).
GN TRPM4B OR TRPM4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RA Perraud A.-L., Scharenberg A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22726392; PubMed=12842017;
RA Hofmann T., Chubakov V., Gudermann T., Montell C.;
RT "TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
RT Selective Cation Channel.";
RL Curr. Biol. 13:1153-1158(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22791733; PubMed=12799367;
RA Nilius B., Prenen J., Droogmans G., Voets T., Vennkens R.,
RA Freichel M., Wissenbach U., Flockerzi V.;
RT "Voltage dependence of the Ca2+ activated cation channel TRPM4.";
RL J. Biol. Chem. 278:30813-30820(2003).
DR EMBL; AF497623; AAM18083.1; -
DR EMBL; AY297045; AAP44474.1; -
DR EMBL; AJ575813; CAB05941.1; -
DR Genew; HGNC:17993; TRPM4.
DR DR; GO:0016021; C:integral to membrane; IEA.
DR DR; GO:0005261; P:cation channel activity; IEA.
DR DR; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; I.
KW Ionic channel; Receptor; Transmembrane.
SQ SEQUENCE 1214 AA; 134300 MW; 76ADA452690ED8F5 CRC64;

Query Match 40.2%; Score 2448.5; DB 4; Length 1214;
Best Local Similarity 45.6%; Pred. No. 7.9e-182;
Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;

Qy 26 GEVNFGGKRGKGFVRVPSGVAPSVLFDLLIAEWHLPAPNLVSVLGVGEQPFAMKSWLR 85
Db 76 GELDTGAGKHSNFRLSDRTPAAVYSLVTRTWGFRAPNLVSVLGVGGGPFVLTWLQ 135
Qy 86 DVLRLKGLVKAAGTGAWILTSALRGLRHVGQAVRDHSLASTKTVRVVAVGMASLGRV 145
Db 136 DLLRLGLVRAAGTGAWIVTGLTGTGRHVGAVRDHQAAGTGTGVVAVGMASLGRV 194

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Qy 146 LHRRIIEAAQEDFPVHY-----PEDGSGSQPLCSLDSNLSHFILVEPBPBGKDGDTLTEL 200
Db 195 RNRDRTLINPKGSPARYRMRGDPED--GVQFP---LDYNSAFELVDDGTHGCLGGENRF 249
Qy 201 RLRLKHIISORAGYGGTGBIEIPVLCLLVNGDPTLERISRAVEQAAPMLILVSGSGIA 260
Db 250 RLRLSEYISQKTVGGTG-IDIPVLLLLIDGDEKMLTRIENATQAOLPCLLVAGSGAA 308
Qy 261 DVLAALVNQPHLLVP-----KVAEKQFKFKSPKSHFSWEDIVRWTKLLQNTITSHOHL 313
Db 309 DCAETLED--TLAPGSGGARQGEARDIRIRFFPK-----CDLEVLQAQVERIMTRKELL 361
Qy 314 TVYDFEQEGSEELDTVLKALVKACKSHSQPPQDYDELKLAIVAMDVRDIAKSIIFNGDV 373
Db 362 TVYSSE--DGSEEPETIVLKALVKAC--GSSEASAYLDELRLAVAWNRVDIAQSELFRGDI 418
Qy 374 EWKSCDLEEVVVDALVSNKBEFVRLFDVNGADVADFLTYGELQELYESVRSKSLLEDLIQ 433
Db 419 QMRSHLEASLMDALLNDRPEFVRLLSHGLSHGFLTPMKLAOLYGAAPSNLIRNLDD 478
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Db 479 QASHSAGTKAPALKGGAELRPP-----DVGHVRLMLLKGMCAPRYESGGAWDPH 528
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Db 529 -----PGQFGESWYLLSDKATSPSLDAGLQAPWSDLLIALLLRAQWAMTFWEMGS 583
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Qy 601 RNRCSWKTTCCLHLATEADAKAFADGVQAFLTRIWMGDMMAAGTPILRLGAFGLCPALV 660
Db 644 RRCPLWGDATCLQAMQADARAFQAQDGVQSLLTQKWGDWASTPIWALVLAFFCPPLI 703
Qy 661 YTNLITP--SSEAPLRTGLELDQLDLSLDTSEKSPYLQSRVEELVEAPRAQGD----- 712
Db 704 YTRLITFRKSEETREELE--FQMDSVINGEPVGTADPAEKTPGLVYPROSGRPGCGG 761
Qy 713 --RGPRAVFLTRWRKKGWAPVTFLGNVNVYAFLEFLTYVLLVDFRPPPGPSGPEVT 770
Db 762 RCGRRRC--LRRFHFWGAPVTIFMGNVVSYLLFLFLFSRVLLVDFQAP--FGSLELL 816
Qy 771 LYFWVFTLVLEBEIRQGFDTEDT-----HLVKKFTLYVGDNNKCDMAIFLFI 819
Db 817 LYFWAFILLCELRQGLSGGGSLASGGPGCHASLSQRLRLYLADSNWQCDLVALTCFL 876
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Db 937 LGVMLVAYGVATEGLLRPRDSDFPSSILRRVFRPVLQIFGQIPQEDMDVALMEHNCNSE 996
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Qy 1043 LPDPLDQKVVWTWTKENFLSKMEKRRDSEGEVLRKTAHRVDFTIAKVLGLIREQEKRI 1102
Db 1117 -----AERKLLTWESVHKENFLARADKRESERLKRSTQKVDLALKQLGHIREYEQRL 1172
Qy 1103 KCLESQINYCSVLSSVADVLAQG-----GGP 1129
Db 1173 KVLREVOQCSRVGLGWAEALSRSALLPPGGP 1204

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RESULT 10
Q7TN37 PRELIMINARY; PRT; 1213 AA.
ID AC Q7TN37
AD Q7TN37
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transient receptor potential ion channel melastatin subgroup member 4
DE protein.
GN TRPM4
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SVJ129; TISSUE=Heart;
RX MEDLINE=22791733; PubMed=12799367;
RA Nilius B., Prenen J., Broogmans G., Voets T., Vennkens R.,
RA Freichel M., Wissenbach U., Flockerzi V.;
RT "Voltage dependence of the Ca2+ activated cation channel TRPM4.";
RL J. Biol. Chem. 278:30813-30820(2003).
DR EMBL; AJ575814; CAB05940.1; -.
KW Receptor.
SQ SEQUENCE 1213 AA; 135759 MW; E4959F53ED35FB66 CRC64;

Query Match 39.4%; Score 2399.5; DB 11; Length 1213;
Best Local Similarity 43.6%; Pred. No. 5.3e-178;
Matches 530; Conservative 185; Mismatches 343; Indels 157; Gaps 30;

QY 26 GEVFGGSGKRGKFRVPSGVAPSLVDFLLAEHLAPNLVSLVSGEEQPFAMKSWLR 85
DB 77 GDLDFYSGKHSNFLRLSDRTPATVYSIVTRSWGFRAPNLVSVLGGSGPVLQTLQ 136
QY 86 DVLRLGLVKAAGSTGAWILTSALRGLARHVGQAVRDHSLASTSTKVRVAVGMASLGRV 145
DB 137 DLLRRGLVAAAGSTGAWIVTGGHTGIRGHVGVAVRDHQTASTGSS-KVAVMGVAPGVV 195
QY 146 LHRRIIEAQEDFPVHY-----PEDGGSGQLCLSDLSNLSHFIVPEPGPKGDLTEL 200
DB 196 RNRDLINPKGFPARYRWGDED--GVEFP--LDVNSAFFVDDTGYRLGGENRF 250
QY 201 RLRLKHXISEAGYGGTSGIPIVLCLLVNGDPNPTLERISRAVEQAAPWLILVSGGITA 260
DB 251 RLRFESYVAQQTGVGGTG-IDIPVLLLLIDGKMLKRIEDATQALQCLLVAGSGGA 309
QY 261 DVLAALVNGPHLLVP-----KVAEKQKFKPPSKHFWEDIVRWTKLLQNTSHOHL 313
DB 310 DCLVETLED--TLAFSGGLRGEARDIRRYFPK-----GDPVLQAQVERIMTRKELL 362
QY 314 TVYDFEQEGSELDVILKALYKACKSHSOEPQDYLDELKLAAMDVDRVDIAKSEIFNGDV 373
DB 363 TVYSSE-DGSEFEFIVIRALVKAC--GSSEASAYLDELKLAAMDVDRVDIAKSEIFRGDI 419
QY 374 EWKSCDLEVMVDALVSNKPEFVRLVDNGADVADFLTYGRQLQELYSRSKSLDFDLQ 433
DB 420 QWRSPHLEASLDALNDRPEFVRLVLSHGLSLGHFLTPVRLAQLYSVSPNSLRNLDD 479
QY 434 RQEEEARLTLGLGTCQAREPAG-----PAFSLHEVSRVLKDFLQDACRGFY----- 482
DB 480 QASH-----ASSSKSPVNGTVELRPP-----NVQVLRITLIGTCAPRYPARNT 524
QY 483 -----QDGRPGDRRAEKGPAKPTGQKWLDDLNQK-----SENPRDLFLWAVLQ 528
DB 525 RDSYLCQDREND-----SLMDWANKQPSDASFEQAFWSOLLWALL 569
QY 529 NRHEMATYFWAMQEGVAAALAAACKILKEMSHLETEAEAAATRE--AKYERLALDLFSE 586
DB 570 NRAQWALYFWKSGNSVASALGACLLRYMARLESEAEAEARRKDLATFESKSVDLFGE 629
QY 587 CYSNSEARAFALLVNRNRCWSTTCLHLATEADAKAPFAHDGVQAFLTRIWGDMAAGTP 646
DB 646 CYSNSEARAFALLVNRNRCWSTTCLHLATEADAKAPFAHDGVQAFLTRIWGDMAAGTP 646

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## RESULT 11

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Q96L84 PRELIMINARY; PRT; 1040 AA.
ID Q96L84
AC Q96L84;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TRP-related cation influx channel (Transient receptor potential cation
DE channel subfamily M member 4 splice variant A).
DE TRPM4.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21438010; PubMed=11535825;
RA Xu X.Z.S., Mosbuis F., Gill D.L., Montell C.;
RT "Regulation of melastatin, a TRP-related protein, through interaction
RT with a cytoplasmic isoform.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:10692-10697(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22726392; PubMed=12842017;
RA Hofmann T., Chubanov V., Gudermann T., Montell C.;
RT "TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
RT Selective Cation Channel.";
RL Curr. Biol. 13:1153-1158(2003).
DR EMBL; AY046396; AAL02142.1; -.
DR EMBL; AY297044; AAP44473.1; -.

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DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005261; P: cation channel activity; IEA.
DR GO: GO:0006812; P: cation transport; IEA.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR005821; Ion_trans.
DR Pfam: PF00520; ion_trans; 1.
KW Ionic channel; Receptor; Transmembrane.
SQ SEQUENCE 1040 AA; 115565 MW; 684A8C554B2B0F2E CRC64;

Query Match 35.5%; Score 2184.5; DB 4; Length 1040;
Best Local Similarity 45.6%; Pred. No. 2.7e-161;
Matches 486; Conservative 156; Mismatches 320; Indels 111; Gaps 26;

QY 125 LASTSTKRVVAVGMAISLGRVLRHRIIEEAQEDFPVHY-----PEDDGGSGQPLCLSDSN 179
DB 1 MASTG-GTKVAVGVAVGVVVRNDDTLINPKGSPFARYWRGDPED--GVQFP---LDYN 54

QY 180 LSHFILVEPPGPGKGGDLTELRLRLEKHISEQRAGYGTGSIETIPVCLLVNGDPNTLER 239
DB 55 YSAFLVDDGTHGCLGGENRFRLESYSQKTVGGTG-IDIPVLLIIDGDEKMLTR 113

QY 240 ISRAVEQAAPWILVSGGIADVLAAALVNQPHLLV-----KVAEQKFEKPSKXFS 292
DB 114 IENATQAQLPCLLVAGSGGAADCLAEITLED--TLAPSGGARQGEARDRIIRFFPK 167

QY 293 WEDIVRWTKLQNTITSHOHLITVYDFEQEGSEELDTVLKALVACKSHSQEPQDYLDL 352
DB 168 -GDLEVLQAQVERIMTRKELLTVYSSE-DGSEEFETIVLKALVKAC--GSSEASAYLDEL 223

QY 353 KLAVAWRDVIJAKSEIFNGDVWVSKCDLEEVNVDALVSNKEFEVRLFDVNGADVADFLTY 412
DB 224 FLAVAWNRVDIAQSELFRGDIQWRSFHLSEASIMDALLNDRPEFVRLIISHGLSLGHFLTP 283

QY 413 GRLQELYSVSRKSLPDLLOKQBEARLTLAGL--GTQQAEREPPAGPAPFSLHEVSRL 470
DB 284 MRLAQLYSAAPSNLIRNLLDQASHSAGTKAPALKGGAELRPP-----DVGHVL 333

QY 471 KDFLQDQACRGYQDGRPDRRRAEKGPAPKRTPGOKWLLDLNQS-----ENPWRDL 521
DB 334 RMLLGKMCAPYPSGAWDPH-----PQGGFESNYLLSDKATPSLSDAGLGQAPWSDL 388

QY 522 FLWAVLQNRHEMATYFWANGQGVAAALAAACKILKEMSHLSEAEARATREA--KVERL 579
DB 389 LLWALLNRAQMAYFWEMGNVSSALGACLLRVWARLPEDAEAAARRKDLAFKPFQM 448

QY 580 ALDLFSECYNSSEARAFALLVRNRCSKTTCLHLATEADAKAPFAHDGVQAFTRIWWG 639
DB 449 GVDLFGECTSRSEVRAALLRRCPLWGDATCLQLAQADARAFPAQGVQSLITQKWWG 508

QY 640 DMAAGTPTILRLGALFCLPALVYTNLITF--SEAPLRTGLEDLQDLSLDTKSPLYGLQ 697
DB 509 DMASTPTIWLALVAFCCPLIYTRLITTFKSEEEPTREELE--PMDSVINGEGVGTAD 566

QY 698 SRVELVEAPRAQD-----RCPRAVFLTRWRKFWGAPVTVFLGNVNYFAFLFLF 749
DB 567 PAEKTPLVGPQRSGRPGCCGCGRRRC---LRRWFHFWGAPVTTFMGNVSYLLFLFLF 623

QY 750 TVLLVLDPRPPQPGSGPEVTLYFWVFTLVLEIRIQGFTEBDT-----HLVKK 798
DB 624 SRVLLVDFQAP--PGSELELLYFWAFILLCEELRQGLSGGGSLASGPGPGCHASLSQR 681

QY 799 FTLVYGDNNKCDMVAIFLVIGVTCRMLPSAFEAGRTVLAMDFVFTLRILHIFAIHKQ 858
DB 682 LRLYLADSWNCDLVALTCFLLGVCRLTPGLYHLGRTVLCIDFVFTVRLIHIETVANKQ 741

QY 859 LQPKLIIVERMKDVEFFFLFSLVWLVAVGYTQALLHPHDCGLEMIFFRVLRYLYQLIF 918
DB 742 LGPKTVIVSRMKDVEFFFLFGLVWLVAVGATEGLLRPRDSFPIILRRVRYLYQLIF 801

QY 919 GQIPLDEIDEARV--NCSTHPLLEDSP-----SCPSLIYANWLIVLLITVTELLVNVLL 970
DB 802 GQIPQEDMDVALMEHNSCSSEFGFWAHPHPGAQAGTCVQYANWLIVLLIVIFLLVANILL 861
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QY 971 MNLLIAMFSYTFQVVGQGNADMFKFORYNLIVEHERPALAPPFILLSHLSLTRRVPKK 1030
DB 862 VLLIAMFSYTFGKVGQNSDLYWKAQRYRLIRFHSRPALAPPFIVISHLRLLRQRCR 921

QY 1031 -----BAEHKREHLERDLPDLPDOKVVTWETQKENFSLSKWEXRRDSECEVLKRT 1081
DB 922 PRSPQSSPALEHFRVYLSKE---AEKLLTWTESVHKENFLARADKESDERLKRT 977

QY 1082 AHRVDTAKYLGRLGRLQEKIKLESQINYCSLVSSVADVLAQG-----GGP 1129
DB 978 SQKVDLALKQLGHIREVEQRLKVLREVOQCSRVGLGWVAELSRALLPPGGP 1030

RESULT 12
Q9NXXV1 PRELIMINARY; PRT; 1016 AA.
ID Q9NXXV1
AC Q9NXXV1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein FLJ20041.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Colon;
RC Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Ota T., Suzuki Y., Ohayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RA "NEDO human cDNA sequencing project."; RT
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000048; BAA90907.1; -.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0005261; P: cation channel activity; IEA.
DR GO: GO:0006812; P: cation transport; IEA.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR005821; Ion_trans.
DR Pfam: PF00520; ion_trans; 1.
KW Hypothetical protein.
SQ SEQUENCE 1016 AA; 113245 MW; F640689A3D94DC6D CRC64;

Query Match 35.5%; Score 2164; DB 4; Length 1016;
Best Local Similarity 45.6%; Pred. No. 1e-159;
Matches 480; Conservative 150; Mismatches 316; Indels 106; Gaps 25;

QY 125 LASTSTKRVVAVGMAISLGRVLRHRIIEEAQEDFPVHY-----PEDDGGSGQPLCLSDSN 179
DB 1 MASTG-GTKVAVGVAVGVVVRNDDTLINPKGSPFARYWRGDPED--GVQFP---LDYN 54

QY 180 LSHFILVEPPGPGKGGDLTELRLRLEKHISEQRAGYGTGSIETIPVCLLVNGDPNTLER 239
DB 55 YSAFLVDDGTHGCLGGENRFRLESYSQKTVGGTG-IDIPVLLIIDGDEKMLTR 113

QY 240 ISRAVEQAAPWILVSGGIADVLAAALVNQPHLLV-----KVAEQKFEKPSKXFS 292
DB 114 IENATQAQLPCLLVAGSGGAADCLAEITLED--TLAPSGGARQGEARDRIIRFFPK 167

QY 293 WEDIVRWTKLQNTITSHOHLITVYDFEQEGSEELDTVLKALVACKSHSQEPQDYLDL 352
DB 168 -GDLEVLQAQVERIMTRKELLTVYSSE-DGSEEFETIVLKALVKAC--GSSEASAYLDEL 223

QY 353 KLAVAWRDVIJAKSEIFNGDVWVSKCDLEEVNVDALVSNKEFEVRLFDVNGADVADFLTY 412
DB 224 FLAVAWNRVDIAQSELFRGDIQWRSFHLSEASIMDALLNDRPEFVRLIISHGLSLGHFLTP 283

QY 413 GRLQELYSVSRKSLPDLLOKQBEARLTLAGL--GTQQAEREPPAGPAPFSLHEVSRL 470
DB 284 MRLAQLYSAAPSNLIRNLLDQASHSAGTKAPALKGGAELRPP-----DVGHVL 333

QY 471 KDFLQDQACRGYQDGRPDRRRAEKGPAPKRTPGOKWLLDLNQS-----ENPWRDL 521
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Db	334	RMLGKMCAPRYPSSGGAWDPH-----PGQFGESMYLLSDKATSPSLDAGLGQAPWSDL	388
QY	522	FLWAVLQNRHEMATYFWAQEGVAAALAAKILKEMSHLETEAEAAARATREA--KYERL	579
Db	389	LLWALLNRAQAMMYFWENGNAVSALLGACILLRVMARLEPDABEAARKDLAFKFGW	448
QY	580	ALDLFSECVNSSEARAFALLVRNRCSKTTCLHLATEADAKAFFAHGQVQAFLTRIMWG	639
Db	449	GVDLFCECVSRSEVRAARLLRCPLWGDATCLQLAMQADARAFFAODQGVQSLLTKWNG	508
QY	640	DNAAGTPIRLLCALCPALVNTLTF--SEAPLRTGLELDLQDLSLDTSEKSPYGLQ	697
Db	509	DNASTPIWALVLAFFCPPLIYTRLTFRKSEEPREELE--FDMDSVINGEGPVGTAD	566
QY	698	SRVEELVEAPRAQGD-----RGPRAVFLTRMRKFWGAPVTYFLGNVVMYFAFLFLF	749
Db	567	PAEKTPLGVPRQSGRCGCCGRCGRCC--LRRWFHFWGAPVTIPMGNNVSYLLFLFLF	623
QY	750	TYVLLVDFRPPQGGSPBVTLYFWYFTLVILVEIRGFFTDDET-----HLVKK	798
Db	624	SRVLLVDFQAP--PGSLBLLYFWAFTLCLBELRQGLSGGGSLASGGPGPGCHASLSQR	681
QY	799	FTYVGVGNWKNCDMVAIFIVGVTCRMLPSAFAEAGRTVLAMDPMVFTLRLHI FAIHQ	858
Db	682	LRLYLADSNQCDLVALTCFLGVGCLRTPGLYHLGRVTLCDPMVFTVRLHLHIFTVVKQ	741
QY	859	LGPKIIVBERMMKDVFFFLFVSVLWVAYGVTTQALLHPHGRLEWIFRVLRYRPLQIF	918
Db	742	LGPKIVIVSKMKDVFFFLFVSVLWVAYGVTTQALLHPHGRLEWIFRVLRYRPLQIF	801
QY	919	GOIPLDEIDARV--NCSTHPLLEDSP-----SCPSLYANWLVILLVITVLLVNTVLL	970
Db	802	GOIPQEDMDVALMEHNSCSSEPGFWAHPGGAQAGTCVSYANWLVILLVITVLLVNTVLL	861
QY	971	MNLLIAMSFTYQVVOGNADMWKEQRYNLYVEYHERPALADPFIILLSHLSLTLRVPFK	1030
Db	862	VNLLIAMSFTYQVVOGNADMWKEQRYNLYVEYHERPALADPFIILLSHLSLTLRVPFK	921
QY	1031	-----EAEHREHLERDLPDLDQKQVWETVQKENFLSKMEKRRDSEGEVLRKT	1081
Db	922	PRSPQSSPALBHFVRLYSKE-----AERKLLTWESVHKENFLILARADKRESERLRT	977
QY	1082	AHRVDFIAKYLGLRQEKRIKLSQINYS	1113
Db	978	SQKVDLALQGHIREYEQRLKVLREVOQCS	1009
RESULT 13			
ID	Q7Z5D9	PRELIMINARY;	PRT; 1069 AA.
AC	Q7Z5D9;		
DT	01-OCT-2003 (TREMBLrel. 25, Created)		
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Transient receptor potential cation channel subfamily M member 4		
DE	splice variant C.		
GN	TRPM4.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22726392; PubMed=12842017;		
RA	Hofmann T., Chubakov V., Gudermann T., Montell C.;		
RT	"TRPMs Is a Voltage-Modulated and Ca(2+)-Activated Monovalent		
RT	Selective Cation Channel."		
RL	Curr. Biol. 13:1153-1158(2003).		
DR	EMBL; AY297046; AAP44475.1; ..		
KW	Receptor.		
SQ	SEQUENCE 1069 AA; 118629 MW; 80DEBD935A55F200 CRC64;		
Query Match			
		34.4%;	Score 2098; DB 4; Length 1069;

Best Local Similarity 41.2%; Pred. No. 1.6e-154;			
Matches 475; Conservative 157; Mismatches 303; Indels 218; Gaps 24;			
QY	26	GEVNTGGSKKGGKFRVPSGVAPSVLFDLLIAEHLPAENLVSVLGVGEQPFAMKSWLR	85
Db	76	GELDTGAGRKSNFLRLSDRTPAAYSLVTRTWGFRAPNLVSVLGGSGGVPVLTQLQ	135
QY	86	DVLRKGLVKAAGSTGAWILTSALRVGLARHVGQAVRDHSLASTSTKRVVAVGMAISGRV	145
Db	136	DLLRGLVRAAGSTGANIVTGLHGTIGHVGVAVRDHOMASTG-CTKVAVGVAWGVV	194
QY	146	LHRRILEEAQEDPPVHY-----PEDGGSGQGLCSLSDSNLSHFLVEPPEPGKGDGLTEL	200
Db	195	RNRDITLNPKGSPARYRWRGDPED--GVQFF--LDYNSAFFLVDDCTHGLCGENRF	249
QY	201	RRLRLEKHISEQAGVGGTSGIEIPVCLLVNGDPTLERISRAVQAAFWILLVSGGGTA	260
Db	250	RRLRLEYSIQKTVGGGTG-IDIPVLLLDIDGEXMLTRIENTAQQLPCLLVAGSGGAA	308
QY	261	DVLAALVNPQHLLVP-----KVAEKQPKFPPSKHFSMEDIVRWTKLONITSHOHL	313
Db	309	DCIAETLED--TLAPSGGARQGEARDIRREFPK-----GDLEVLQAVRIMTRKELL	361
QY	314	TYVDFEQEGSEELDTVILKALYKACKSHSQEPQDYLDLKLAVAMDVRDIAKSEIPNGDV	373
Db	362	TVYSSE-DGSEEFETIVLKVKAC--GSSEASAYLDELRLAVAMRVVDIAQSELFRGDI	418
QY	374	EWKSCDLBEVMYDALVSNKPEVRFLVDNGADVADPFLTYGRLOELYRSVRSKLLFDLQ	433
Db	419	QWRSHLEASLMDALNDRPEFVRLISHGLHFLTPMLAQLYSAAPSLSLRNLAD	478
QY	434	RKQBEARLTLAGL--GTQAREPPAGPAPAFSLHESVRLKDFLQACRFGYQDGRGRR	491
Db	479	QASHAGIKAPAKLKGAAELRPP-----DVGHVLRMLLKKMCAPIRYSGGAWDPH	528
QY	492	RAEKGPAPKPTGQKWLDLNOKS-----ENPWRDLFLWAVLQNRHEMATYFWAQ	542
Db	529	-----PGQFGESMYLLSDKATSPSLDAGLGQAPWSDLLWALLNRAQAMMYFWENG	583
QY	543	EGVAAALAAACKILKEMSHLETEAEAAARATREA--KYERLALDLFSECVNSSEARAF	600
Db	584	NAVSSALGACILLRVMARLEPDABEAARKDLAFKFGGVDLFGECYRSSEVRAARLL	643
QY	601	RNRCSKTTCLHLATEADAKAFFAHGQVQAFLTRIMWGDMAAGTPILRLCAFLCPALV	660
Db	644	RACPLWGDATCLQLAMQADARAFFAODQGVQSLLTKWNGDMASTTPIWALVLAFFCP	703
QY	661	YTNLTLP--SEAPLRTGLELDLQDLSLDTSEKSPYGLQSRVEELVEAPRAQGRPRAV	718
Db	704	YTRLITFRKSEEPREELE--FDMDSVINGEGP-----	735
QY	719	FLTLTRKFWGAPVTYFLGNVVMYFAFLFTYVLLVDFRPPQPGSPGPEVTLYFWVFTL	778
Db	736	-----	735
QY	779	VLEIRQGFFTDEDTHLVKKFTLYVGDNNWKNCDMVAIFLIVGVTCRMLPSAFAEAGRTV	838
Db	736	-----VGLT-----PGYHLGRVTL	750
QY	839	AMDFMVFTLRLHI FAHKQGPKIIVVERMMKDYFFFLFSLVWLVAYGVTTQALLHPH	898
Db	751	CIDFMVFTVRLHIFTVNKQGPKIVIVSKMKDVFFFLFSLVWLVAYGVATEGLRPR	810
QY	899	DGRLEWIFRVLRYRPLQIFQGIPLDEIDARV--NCSTHPLLEDSP-----SCPSLY	950
Db	811	DSDFPSILRRVFRYPYLQIFQGIQEDMDVALMEHNSCSSEPGFWAHPGGAQAGTCVSY	870
QY	951	ANWLVLLVITVLLVNTVLLMNLIIAMFSYFQVVOGNADMWKEFORNLYVEYHERPAL	1010
Db	871	ANWLVLLVITVLLVNTVLLMNLIIAMFSYFQVVOGNADMWKEFORNLYVEYHERPAL	930
QY	1011	APPFILLSHLSLTLRVPFK-----EAEHREHLERDLPDLDQKQVWETVQKEN	1061



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Db 931 APPFIVISHURLLRQLCRPRSPQSPSPALEHFRVYLSKE-----ABRKLLTWESVHKN 986
Qy 1062 FLSQWKKRRSDSEGEVLKTAHRVDFTAKYVGLGLREOEKRIKLCLESQINVCVLSVSSVAD 1121
Db 987 FLIARADKRSDESERUKRTSKQKVDLALKQLGHIREYQRLKVLREVOQCSRVLGVWAE 1046
Qy 1122 VLAQG-----GGP 1129
Db 1047 ALSRSALLPEGP 1059

RESULT 14
Q8BLM7
ID Q8BLM7 PRELIMINARY; PRT; 945 AA.
AC Q8BLM7
DT 01-MAR-2003 (TremBrel. 23, Created)
DT 01-MAR-2003 (TremBrel. 23, Last sequence update)
DT 01-JUN-2003 (TremBrel. 24, Last annotation update)
DE Similar to TRP-related cation influx channel.
GN 1110030C19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA the FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).
DR EMBL; AK044034; BAC31771.1; -
DR MGD; MGI:1915917; 1110030C19RIK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002111; Cat channel_TripL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
SQ SEQUENCE 945 AA; 105526 MW; B7261C03A6B866EB CRC64;

Query Match 34.0%; Score 2069; DB 11; Length 945;
Best Local Similarity 45.8%; Pred. No. 2.4e-152;
Matches 455; Conservative 141; Mismatches 274; Indels 124; Gaps 27;

Qy 100 GAWILTALRVGLARHVQAVRDHSLASTSTKRVVAVGMASLGRVLRHRLIEBAQEDFP 159
Db 4 GAWITVGLHTGIGHVGVAVRDHQTASTGSS-KYVAVGVAPWGVVRNDRMLINPKGSFP 62
Qy 160 VHY-----PEDDGSQGLCSLDSNLSHFILVEPGPGKDGTLRLRLLEKHISEQRAQ 214
Db 63 ARYWRGDPE--GVEFP---LDVNSYAFFLVDDGTGYRLGENFRFRFESYAAQQTG 117
Qy 215 YGGTGSIEIPVCLLVNGDPNLTLEISRAVEQAAPWLLVGGGIADYLAALVNPQPHLV 274
Db 118 VGGTG-IDIPVLLLLIDGDKMLKRIEDATQALPCLLVAGSGGAADCLVETLED--TLA 174
Qy 275 P-----KVAEKQFKEFPKHSWEDIVRWTKLLQNLITSHOHLITVYDFEQEGBELD 327
Db 175 FSGGLRRGEARDIRRYFPK-----GDPEVLQAQVERIMTKELLTYYSSE-DGSEBFE 228
Qy 328 TVILKALVKACKSHQEPQDYDELKLVAMDRVDIAKSEIFNGDVENKSCDLEVMVDA 387
Db 229 TIVRALVKAC--GSSEASAYLDELRLAVANNRVDIAQSELPFGDIQWRSPHLEASLMDA 286
Qy 388 LVSNKPEFVRFLVNGADVADFLTYGRLOEYLRSVRSKSLFLDLIQRKQEARLTLAIGL 447
Db 287 LLNDRPEFVRLIIHSLGHFLTPVRLAQLYSAVSPNSLRNMLDQASH----- 336
Qy 448 TQAREPPAG-----PPAFSLHESVRVLKQFLODQACRGFY-----QDGRPGR 490
:: :: ||| ( : : : : : )

```



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DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF00293; NUDIX; 1.
DR PROSITE; PS00092; N6_MTASE; 1.
KW Ionic channel; Receptor; Transmembrane.
FT NON_TER 1507 1507
SQ SEQUENCE 1507 AA; 172364 MW; 86E552DE25939785 CRC64;

Query Match      33.2%; Score 2021; DB 11; Length 1507;
Best Local Similarity 39.1%; Pred. No. 2.9e-148;
Matches 449; Conservative 193; Mismatches 386; Indels 120; Gaps 22;

QY 26 GEVNFSGSKKGRKFRVPSGVAPSVLFDLLAEWHLPAFNVLVSLVGEQPFAMKSWLR 85
Db 127 GDIVFTDLQKGVKVRVSDTSSVIYQLMTQHWGLDVPNLLISVTGAKNFNMKLRUK 186
QY 86 DVLRLKGLVKAQSTGAWILTSALRUGLARHVGQAVRDHSLASTSTKRVVAVGMASLGRV 145
Db 187 SIFRRGLVKAQTTGAWIITGGSHTGVMKQVGVAVRDFSLSSCKEGETIIGVATWGTI 246
QY 146 LRRRILEEAEQEDPPVHYHEDDGGSGQPLCSLDNSLHFIIVPEPGPKGDGLTELRLLE 205
Db 247 HNRGLIHMPGFPAPYMLDEEG-QGNLTCLDSNHSHFILVDDGTGQYGVETPLRTKLE 305
QY 206 KHISEQAGYGGTSGTIEIPVLCLLVNGDENTLERISRAVEQAAPWLILVSGGGIADVLAA 265
Db 306 KFISEQTKERGGV-AIKIPICVVLGGPGTLLHTIYNAINNGTFCVIVEGSGRVADVIAQ 364
QY 266 LVNQP--HLLVPKVAEQ---FKEKFPKHSWEDIVRTKLLONITSHQHLITVYDFEQ 320
Db 365 VATLPVSEITISLIQOKLSIFFQEMFET--FTENQIVEMWTKIQDIVRRRQLTIIFREGK 422
QY 321 EGSEELDTVILKALVKACKSKSQEPDYL-DLKLAVANDRVDIAKSEIIFNGDVEWMSKD 379
Db 423 DGQODVDVAILQALLKASRSQDFHGENWDHQKLAVANRVVDIARSEIFTDEWQMKPAD 482
QY 380 LEEVMVALSVNKPFEVRLFDVNGADVADPLTYGRQLQELYSVSRKSLFLDLIQR-KQEE 438
Db 483 LHPMTAALISNKPFEVRLFLENGVRLKEFVTWDTLLCLYENLEPSCLFHSKLQKVLAE 542
QY 439 ARLTLAGLTQQAEPAPGAPFAPSLHEVSRVLKDFLODAGRFPYQGRPGCDRRRAE---- 494
Db 543 QRLAYA-----SATPRLHMHHVAQVLRELLGSDTQLLYPRPYTDRPRLSMTVP 591
QY 495 -----KGPAKRPYTGQ-KWLLDLNOKSENPRDLFLMAVLONRHEMATYFWAMGQ 542
Db 592 HIKLVQGVSLRSLYKRSTGHVTFITD-----PVRDLIWAIVQNHRELAGIHWAAQ 644
QY 543 EGVAAALAAACKILKEMSHLE--TEAFAARATREAKYERIALDLDFSECYNSSEARAFALIV 600
Db 645 DCTAAALACSKILKELSEKEEDTDSSEEMALADEFEHRAIGVFTCYRKDEERAQKLIV 704
QY 601 RNRCKSKTCLHLATEADAKAFFAHDGVOAFLTRIWDGDMAGTPIRLGLAFLCPALV 660
Db 705 RVSEAMGKTTCLQALEAKDMKFVSHGGIQAFLTKVMWGQLCVDNGLMRLIILCMLAFPLL 764
QY 661 YTNLITFSEAPLRTGLEDLQDLSDLTEKSPLYGLQSRVEELVEAPRAQGRGPRAVFL 720
Db 765 FTGFTISFREK-----RLQALCRPARV----- 785
QY 721 LTRWRKFWGAPVTVFIGNVVMYPAFLFTYVLLVDPRPPQPGSPGVETLYFWVFTVLV 780
Db 786 ----RAFFENAPVVFHNNILSYFAFLCLFAYVLVDFQP---SPSWCEVLIIVLWLPFLVC 838
QY 781 EELRQGFPTDED--THLVKFTLYVGNWNKCDMWAIPLFIVGTCTMLPSAFEAGRTVLA 839
Db 839 EETRQVLFYDPPDGGCLMKMASLYPSDFWNKLDVGAILLFIIVGLTCRLIPATLYPGRIILS 898
QY 840 MDMFWETLRLIHFAIHKOLGPKIIVVERMKDVREFLEPFLSVLVAYGVTTQALLPHD 899
Db 899 LDFIMECLRMHLFTISKTLGPKIIIVKRMKDVFFFLFLLAVVWVSVFGVAKQAILHNE 958
QY 900 GRLEWIFRVLXRPYLQIFGQIP--LDEIDEARVNC-----THPLLLEDSPSCPS----- 948
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Search completed: September 14, 2004, 00:06:08  
Job time : 77 secs

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Db 959 SRVDMIFRGVYHSYLTIFGQIPTIYDGVNFSMDQCSPNGTDY-----KPKCESDWTGQ 1014
QY 949 --LIYANWLIVLLIVTELLVTNVLNMLLIAMPSYTFQVVGQGNADMFWKFORYNLIVEYHE 1006
Db 1015 APAPPEWLTVTLLCLYLLFANILLNLLIAMFNFTQEQVQHTDQIWKFORHDLIBEYHG 1074
QY 1007 RPALAPPFILLSHLSLTLRVFKKEAEHREHLERDLPDLDQKVVTWETVQKENFLSKM 1066
Db 1075 RPAPPPLILLSHLQLLIRIVLIPAKRHQKJNKLENEETALLUSWELYLKENYLNQ 1134
QY 1067 EKRRDSEGEVLRKTAHRVDFIAKYL-----GGLREQEKRICKLESQINYGSVLVSSV 1119
Db 1135 QYQOKQRPQKIQIDISEKVDITWVDLLDMQVKRSGSTEQ--RLASLEEQVTVTRALHWI 1192
QY 1120 ADVLAQGG 1127
Db 1193 VTTLKDSG 1200
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 14, 2004, 00:03:08 ; Search time 23 Seconds  
(without alignments)  
2614.968 Million cell updates/sec

Title: US-10-026-188-8

Perfect score: 6093

Sequence: 1 MDVQCPRPSPGDAEDRR.....HRGLDGEQPGAGPPSDT 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/aaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/aaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/aaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/aaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/aaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/aaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2039	33.5	1503	4	US-09-600-087-2
2	1566.5	25.7	1095	3	US-09-112-096-15
3	1566.5	25.7	1095	4	US-09-636-215-778
4	1566.5	25.7	1095	4	US-09-685-166A-778
5	1558.5	25.6	1095	4	US-09-636-215-780
6	1558.5	25.6	1095	4	US-09-685-166A-780
7	1240.5	20.4	1533	1	US-08-623-679-9
8	1240.5	20.4	1533	3	US-08-933-774-9
9	1240.5	20.4	1533	3	US-09-181-030-9
10	1240.5	20.4	1533	4	US-09-534-242-9
11	1240.5	20.4	1533	4	US-09-454-854-9
12	1240.5	20.4	1533	4	US-09-164-671-9
13	1162.5	19.1	1497	1	US-08-623-679-7
14	1162.5	19.1	1497	3	US-08-933-774-7
15	1162.5	19.1	1497	3	US-09-181-030-7
16	1162.5	19.1	1497	4	US-09-534-242-7
17	1162.5	19.1	1497	4	US-09-454-854-7
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22	820	13.5	315	4	US-09-352-616A-112
23	820	13.5	315	4	US-09-232-149A-112
24	820	13.5	315	4	US-09-159-812-112
25	820	13.5	315	4	US-09-636-215-112
26	820	13.5	315	4	US-09-685-166A-112
27	820	13.5	315	4	US-09-115-453-112

US-09-600-087-2  
; Sequence 2, Application US/09600087  
; Patent No. 6548272  
; GENERAL INFORMATION:  
; APPLICANT: Shimizu, No. 6548272uyoshi  
; TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN  
; FILE REFERENCE: 11283-004001  
; CURRENT APPLICATION NUMBER: US/09/600,087  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: PCT/JP99/06289  
; PRIOR FILING DATE: 1999-11-11  
; PRIOR APPLICATION NUMBER: JP/321200/1998  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1503  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: TRANSMEM  
; LOCATION: (320)...(344)  
; NAME/KEY: TRANSMEM  
; LOCATION: (750)...(773)  
; NAME/KEY: TRANSMEM  
; LOCATION: (794)...(818)  
; NAME/KEY: TRANSMEM  
; LOCATION: (867)...(891)  
; NAME/KEY: TRANSMEM  
; LOCATION: (900)...(924)  
; NAME/KEY: TRANSMEM  
; LOCATION: (932)...(956)  
; NAME/KEY: TRANSMEM  
; LOCATION: (1024)...(1048)  
US-09-600-087-2

#### ALIGNMENTS

#### RESULT 1

US-09-600-087-2  
; Sequence 2, Application US/09600087  
; Patent No. 6548272  
; GENERAL INFORMATION:  
; APPLICANT: Shimizu, No. 6548272uyoshi  
; TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN  
; FILE REFERENCE: 11283-004001  
; CURRENT APPLICATION NUMBER: US/09/600,087  
; PRIOR FILING DATE: 2000-07-11  
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; PRIOR APPLICATION NUMBER: JP/321200/1998  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1503  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: TRANSMEM  
; LOCATION: (320)...(344)  
; NAME/KEY: TRANSMEM  
; LOCATION: (750)...(773)  
; NAME/KEY: TRANSMEM  
; LOCATION: (794)...(818)  
; NAME/KEY: TRANSMEM  
; LOCATION: (867)...(891)  
; NAME/KEY: TRANSMEM  
; LOCATION: (900)...(924)  
; NAME/KEY: TRANSMEM  
; LOCATION: (932)...(956)  
; NAME/KEY: TRANSMEM  
; LOCATION: (1024)...(1048)  
US-09-600-087-2

Query Match 33.5%; Score 2039; DB 4; Length 1503;

Best Local Similarity 38.8%; Pred. No. 1.1e-190;

Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

QY 26 GEVNFSGKRGKFKFVRVPSGVAPSLFDLLIAEHLFAPNLVSLVGEQPFAMKSLR 85

DB 128 GDIVFTGLSQKVKVVRVSDTPSPSVIHLMTQHGLDVENLLISVTGAKNFNMKPRLK 187

QY 86 DVLRLGLVKAAGSTCAWILTSALRLVGLARHVGOAVRDLASTSTKVRVAVGVMSLGRV 145

DB 188 SIFRRGLRVKAQTGTGTAIITGSHSTGVNMQVGEAVRDFSLSSSYKEGLITIGVATGTV 247

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146 LHRRLIEEAQDFPHVHPEDGGQGLCSLSDSLSHFVLVPEPPGKGDLGLTELRLE 205
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248 HRREGLIHTPTGSFPAEYILDEBG-QGNLTCLDSNHSFILVDDGTHGQYGEIPLRTELE 306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
206 KHISEQAGYGTGSIEIPVCLLVGNDPNTLERISRAVEQAAPWLIVGSGGIADUAA 265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
307 KFISEQTKERGCV-AIKPIVCVVLGGPGGLTHIDNATNGTFCVVVGGSGRADVIAQ 365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
266 LVNOP--HLLVPKVAEQ--FKEKFPKSHFSDIVRWTKLQNTSHOHLTYVDPEQ 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
366 VANLPVSDITISLTOQLSVFQEMFET--FTESRIVENTTKIIDIIVRRQILLVREGK 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
321 EGSEELDTVILKALVKACKSHSQEPQDYLDELKLA VAWDRVDAKSHIFNGDVEWKS 379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
424 DQGDVDVAILQALLKASRSQDHFGHENWDLKLA VAWNRVDIARSEIFMDEWQKPSD 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
380 LEEVMDALVNKPEFVPLFVNDGADVADFTYGLQELYSVSKSLFLLQKQBEA 439
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
484 LHPTMTAALISNKPEFVKFLFENGVLKEFVTWDTLLYENLDPSCFLFHSKLOK---- 538
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440 RLTLAGLTQOAREPPAGP--PAFSLHEVSVRLKDFLQDACKGFYQDGRGPRDRR---- 492
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539 -----VLVDEPERPACAPAPRLQMHVAVQLRELLGDTFQPLYPRHNDRLRLLPV 592
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493 -----AEKGPARKPTQOKMLLDLNQKSENPWRDLFLWAVLQNRHEMATYFWAMQ 542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
593 PHVKLVQGVSLRSYKSSGHVTF-----TMDPIRDLIIWAIQNRRELAGIIWAQSQ 646
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
543 EGVAALAAACKILKEMSHLETAEAR--ATRAKVERLALDLFSECVSSEARAFALL 599
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647 DCIAAALACSKILKELKEEDTSSSEMLALAE-EYEHRAIGVFTECYRDEERAQKLL 705
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600 VRRNRCWTKTCLHLATEADAKAFPAHDGVQAFTRIWWGDMAAGTPTLRLGLAFLCPAL 659
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706 TRVSEAWGKTCQLALEAKDMKPVSHGGIOAFLTKVWVGQLSVNDGLWRVTLCLMFLPL 765
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
660 VYTNLITFSEAPLRTGLEDLQDLSLDTESKPLGLQSRVEELVEAPRAQDGRPAVF 719
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766 LLTGLISPREKR-----LQD-----VGTFAA----- 786
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720 LLTWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDRPPPPQSGSEVTLTYFVFTLV 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
787 ---RARAEFTAPVVVTHUNILSYFAFLCLFAYLWVDFQPV---PSWCECAIYLMFLSV 840
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780 LEEIRQGFDTDETHLVKKFTLYVGDNNWKNCDMAIFLIVGVTCRMLPSPAFAEAGTVLA 839
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841 CEEMRQLFYDDECGLMKKAALFYSDFNKLDVGAILLVAGLTCRLIPATLYPGRVILS 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
840 MDPVFTLRLTHIFAIHQKGPKEIIVVERMKDVFFFLFSLVMLVAYCVTTOALLHPHD 899
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
901 LDFILFCRLMHIFTISKTGLPKIIVKRMKDVFFFLFLLAVVWVSGVAKQAILHNE 960
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
900 GRLEIFRRVLYRYPYQIFGQIP--LDBIDEARVNCS---THPILLEDSPSCPS----- 948
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961 RRVDMLFGAVYHSLTIFGQIPGYIDGVNPNFCHSCSNGTDPY----KPKCPSPDATQQ 1016
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949 ---LYANWILVLLVTLVNTVLLMNLIIAMFSYTFVQVQGNADMFWKFORNYLIVEYHE 1006
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1017 RPAPEWLVLLCLLYLFTNILLNLLIAMFNVTYFQVQBHTDQIKWFORHDLIEEYHG 1076
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1007 RPALAPPETLISHLSLTLRRVFKAEKREHLERDLPDLDQKVVTWETQKNFSLMS 1066
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1077 RPAAPPPETLISHLQLFTRVVVLTTPAKRHQKLNKLEKNEAALLSWEIYLKENYLNQR 1136
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1067 EKRARDSGEVLRTAHVRDVFIAKYL-----GGLREQEKRIKLESQINYSVLVSS 1118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1137 QFOQKQREPEQKIEDISNKVDAMVDLLDPLKRSQSM---BQRLASLEEQAQARALHW 1193
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1119 VADVIAQGGGRSSQHCQGGSQLVAAD---HRGGLDGWEQPG 1157
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1194 IVRTLRSQFSGSEADVPTLASAKAAEPEDAEPGGRKTEEPG 1235
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RESULT 2
US-09-112-096-15
; Sequence 15, Application US/09112096
; Patent No. 6194152
; GENERAL INFORMATION:
; APPLICANT: Reinher Laus
; APPLICANT: Michael H. Shapiro
; APPLICANT: Larisa Tsavaler
; TITLE OF INVENTION: Prostate Tumor Polynucleotide and
; TITLE OF INVENTION: Antigen Compositions
; FILE REFERENCE: 7636-0015.30
; CURRENT APPLICATION NUMBER: US/09/112,096
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: 60/056,110
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-112-096-15

Query Match      25.7%; Score 1566.5; DB 3; Length 1095;
Best Local Similarity 34.3%; Pred. No. 2.2e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

QY 26  GEVNFSGGKKRGKRVFVPSGVAPSVLFDLLLAELWHLPAFNLVSVLVEEQPFAMKSWLR 85
DB 95  GDIOFETLGGK-GKVIKSLCDDTAELIYELLTQHHLKTPNLVSVTGVAKNFALKPMR 153
QY 86  DVLKGLVKAQSTGAWILTSALRVGLARHVQAVRQHSLASTSTKRVVAVGVASLGRV 145
DB 154 KIFSR-LIYTAQSKGAWILTGTHYGLTKYIGEVVRDNTI--SRSEENIVAGIAAGMV 211
QY 146 LHRRIE---BAQEDFPVHYPEDGGQGLCSLSDSLSHFVLVPEPPGKGDLGLTEURL 202
DB 212 SNRDTLRNCDAGYFLAQYLMDD-FTRDPLIYLDNNHHTLHLLVNDGCHGHTPEAKURN 270
QY 203 RLEKHISE---QRAGYGGTGSIEIPVCLLVNGDPNTERISRAVEQAAPWLIIIVGSGGI 259
DB 271 QLEKHISERTIQDSNYG---KIPVCFAGGGGKETLKAINTSIKNKPCVVVEGSGRI 326
QY 260 ADVLAAIVNQPHLLVPKVAEKQKFPFS--KHSWEDIVRWTKLQNTSHOHLTYVD 317
DB 327 ADVIASLVEVDAPTSSAVKKEKLVRFPLRPTVSRLSSEETESWIKWKEILKCSHLLTVIK 386
QY 318 FEQSGSELDIVILKALVKACKSHSQEPQDYLDELKLA VAWDRVDAKSHIFNGDVEWKS 377
DB 387 MEEAGDEIVSNAIYALYKAFSTSEQDKNNWGLKLELWNLQDLNDEIFTNDRWES 446
QY 378 CDLEVMVDALVSNKPEFVPLFVNDGADVADFTYGLQELYSVSKSLFLLQLQ---R 434
DB 447 ADLQEVMTALIKDRPKFVRLFLEGLNLRKFLTHDVLTELF-SNHFTSLVYRNLIQAKN 505
QY 435 KQESARITLAGLGTQOAREPPAGPAPSLHVSRLKDFLQDACKGFYQDGRPG-DRRRA 493
DB 506 SYNDALLTF-----VWKLVANFR---RGRFRKDRNGRDEMDI 539
QY 494 EKGPAKPTGQKWLLDLNQKSENPRDLFLWAVLQNRHEMATYFWAMQEGVAAALAAACK 553
DB 540 E-----LHDVSPITRPLQALFIWAILQNKKELSKVIWEQTRGTGTLAALGASK 587
QY 554 ILKEMSHLETBAEAARATREA--KYERLALDLFSECVSSEARAFALVRRNRCWSKTTC 611
DB 588 LLKTLAKVNDINAAGESEELANEYETRAVELFTECYSSDEDLAEQLLVYSCAAMGSGNC 647
QY 612 LHLATEADAKFAHGDGVQAPLTIWGDMAAGTPTLRLGLAFLCPALVYTNLITFSEEA 671
DB 648 LELAVEATDQHTAQPGVQVNFSLKQWYGETSRDTKNWKIILCLFTIPLVGGGFSFRKK- 706
QY 672 PLRTGLEDLQDLSLDTESKPLGLQSRVEELVEAPRAQDGRPAVFLLTRWRKFWGAP 731
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Db 707 -----PVDKHK-----LLWYVAFFTSP 725  
Qy 732 VTVELGNVYFAFLFTYVLLVDRPBPQSPGSEVTLVFWFTLVLEERQGFTE 791  
Db 726 FVFSNWNVYFAFLFTYVLLVDRPBPQSPGSEVTLVFWFTLVLEERQGFTE 782  
Qy 792 DTHLVKFTLYVGDNNKCDMAIFLIVGVTCRM---LPSAFEAGRTVLAMDPMVFTLR 848  
Db 783 N-----YFTDLNWNMDTLGLFYAGIVFRLHSSNKSSLYSGRVFCLDIYFTLR 833  
Qy 849 LHIHFAIHKQLGPKIIVVERMMKDVFFFLFSLVNLVAVGVTTQALLPHDGRLEWIFRR 908  
Db 834 LHIHFTVSRNLGPKIIMQLMLIDVFFFLFSLVNLVAVGVTTQALLPHDGRLEWIFRR 893  
Qy 909 VLYRPYLIQFQIPLDEIDEAR---VNCS-----THPLLE-DSPSCPSLYANWLVLILL 959  
Db 894 VIYEPYLAAMFGQVPSD-VDGTTYDFAHCTFTGNEKPLCVELDEHNLP-FFEWITPIV 951  
Qy 960 VTFLVTVNLLMNLIAFMSYTFQVVGADMFQKFORNLVIEYHERPALAPPFILLSH 1019  
Db 952 CIYMLSTNILLNVLVAMFGYTVGVQENNDQVWKFORVFLVQVCSRLNIPFFIVPAY 1011  
Qy 1020 LSLTLRRVPKKAHREHLERDLPDLPQKVVTVWETVOKENFLSKMEKRRDSEGEVLR 1079  
Db 1012 FYWVVKCKCFCKCKEKNMSESSVCCFKNEDNETLAWGVKENVLYKINTKANDT-SEEMR 1070  
Qy 1080 KTAHRVDFIAKVLGG-LRQEKRIK 1103  
Db 1071 HRFRLDQTKLNDLKGILLKIANIK 1095

## RESULT 3

US-09-636-215-778  
; Sequence 778, Application US/09636215  
; Patent No. 6620922  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqui  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636,215  
; NUMBER OF SEQ ID NOS: 852  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 778  
; LENGTH: 1095  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-636-215-778

Query Match 25.7%; Score 1566.5; DB 4; Length 1095;  
Best Local Similarity 34.3%; Pred. No. 2.2e-144;  
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;  
Qy 26 GEVNFSGSKRGKFRVRSVGVAPSVLFDLLIAEHLDPNLVSVLUGVEQPFAMKSWLR 85  
Db 95 GDIQFETLGGK-GKYLRLSCDTEAELLYELLTQHHLKTPNLVLSVTVTGAKNFALKPRMR 153

Qy 86 DVLKGLVKAQSTGAWILTSALRVGLARHVGQAVRDHSLASTSTKRVVAVGMSILGRV 145  
Db 154 KFSR-LIYIAQSKGAWILTGTHGLTKYIGEVVDNTI-SRSEENIVAIGAWMV 211  
Qy 146 LHRRIE-----EAQDFFPVHYPDDGSGQGLCSLDSNLSHFILVPEFGPKGDLTELR 202  
Db 212 SNRDTLIRNCDAEGVFLAQYLMDD-FTRDPLVLDNNHNLHLLVDNGCHGHPTEAKLRN 270  
Qy 203 RLEKHISE---QVAGYGGTGSIEIPVLCLLVNGDPNTERISRAVEQAAPWLLVCSGGI 259  
Db 271 QLEKHISERTIQDSNYGG---KIPVCEAQQGKETLKAINTSIKNKPCPVVVEGSGRI 326  
Qy 260 ADVLAALVNOPHLLVPKAEKOFKEKFPs---KHFSWEDIVRWTKLONITSHOHLITVYD 317  
Db 327 ADVIASLVEVEDAPTSASVKEKLVFLPRTVSRLESEETESIKWLKEILECSHLITVVK 386  
Qy 318 FQEGSEELDTVILKALVKACKSHSQEPQDYLDLKLAVANDRVDIAKSEIFNGDVEWKS 377  
Db 387 MEEAGDEIVSNAISVALYKAFSTSEQDKDNWNGQLKLLLEWQLDLANDEIFTNDRRES 446  
Qy 378 CDEEVMWDALYSNKPFRVLFVDNGADVADFLTYGRLOELYRSVSRKSLLPDLQ---R 434  
Db 447 ADLQVEMFTALIKORPKFVRLFNGLNLRKFLTHDVLTELF-SNHFTSLVTRNLQIAKN 505  
Qy 435 KQBEARLTLAGLGTQARPPAGPPAFSLHSEYSRVLKDFLQDACRGFYQDGRPG-DRRA 493  
Db 506 SYNDALLTF-----VWKLVANFR-----RGFKEDNRGRDEMDI 539  
Qy 494 EKGAKRPTGQKWLDDLNOKSNPNWRDLFLWAVLQNRHEMATYFWAMGEGVAAALAAK 553  
Db 540 E-----LHDVSPITRHLQALFIWAILQNKELSKVIMEQTRGCTLAALGASK 587  
Qy 554 ILKEMSHLETEAARAATFEA--KYERLALDLFSECYSNSEARAFALLVRRNRCWKTTC 611  
Db 588 LIKTLAKVNDINAAAGESEELANETRAVELTECYSSDEDLAEQLLYSCEAWGSGNC 647  
Qy 612 LHLATEADAKAFFADHGVQAFLTRIWWGDMAGTPTILRLGLAFLCPALVYVNLITSEEA 671  
Db 648 LELAVEATDQHTAQTGQVGNFLSKQWYGEISDRTKNWKLILCLFIPLVGGCFVFRKK- 706  
Qy 672 PLRTGLELDQLDLSLDEKSPLYGLQSRVEELVEAPRAQGDGRPAVFLTLTRKRFWGP 731  
Db 707 -----PVDKHK-----LLWYVAFFTSP 725  
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Qy 849 LHIHFAIHKQLGPKIIVVERMMKDVFFFLFSLVNLVAVGVTTQALLPHDGRLEWIFRR 908  
Db 834 LHIHFTVSRNLGPKIIMQLMLIDVFFFLFSLVNLVAVGVTTQALLPHDGRLEWIFRR 893  
Qy 909 VLYRPYLIQFQIPLDEIDEAR---VNCS-----THPLLE-DSPSCPSLYANWLVLILL 959  
Db 894 VIYEPYLAAMFGQVPSD-VDGTTYDFAHCTFTGNEKPLCVELDEHNLP-FFEWITPIV 951  
Qy 960 VTFLVTVNLLMNLIAFMSYTFQVVGADMFQKFORNLVIEYHERPALAPPFILLSH 1019  
Db 952 CIYMLSTNILLNVLVAMFGYTVGVQENNDQVWKFORVFLVQVCSRLNIPFFIVPAY 1011  
Qy 1020 LSLTLRRVPKKAHREHLERDLPDLPQKVVTVWETVOKENFLSKMEKRRDSEGEVLR 1079  
Db 1012 FYWVVKCKCFCKCKEKNMSESSVCCFKNEDNETLAWGVKENVLYKINTKANDT-SEEMR 1070  
Qy 1080 KTAHRVDFIAKVLGG-LRQEKRIK 1103  
Db 1071 HRFRLDQTKLNDLKGILLKIANIK 1095





203 RLEKHISE---QRAGYGGTGSIEIPVLVLLVNGDPNTLERISRAVEQAAPMLLIVGGGI 259  
271 QLEKVIISERTIQDSNYG---KIPVCFAGGGKETLKINTSIKNKIPCVVVEGSGQI 326  
260 ADVLAALVQPHLLVPKVAEQKPEKPS---KHFSWEDIVRTWTKLQNTSHQHLITVYD 317  
327 ADVIASIVEBALDTSAAVKEKLVRFPLRTVSRLPSEETESWIKWKEILKESHLITV 386  
318 FEQEGSELDVTILKALVKACKSHSQBPQDYLDELKLAAMDVRDIAKSEIFNGDVWKS 377  
387 MEEAGDRIVSNALSYALYKAFSTEQDKDNWNGQLKLELWQDLDLNDLDEIFTNDRWES 446  
378 CDLEVMVDALVSNKPFVRLFVDNGADVADFLTYGRLOELYSRVSRSKSLFDLLQ---R 434  
447 ADLQEVMTALIKDRPKFVRLFENGLNLRKFLTHDVLTELF-SNHFSSTLYRNLQIAKN 505  
435 QOEERARITLAGLGTQOAREPPAGPAPSLHEVSRVLDFQDACRGFYQDORPG-DRRA 493  
506 SYNDALLTF-----VWKLVANFR---RGRKEDRNGRDEMFI 539  
494 EKGPAKPTGOKWLLDLNOKSENPRDLFLWAVLQNRHEMATYFWAMQOEGVAAALACK 553  
540 E-----LHDVSPTRHPQLQALFIWAILQNKELSKVINEQTRGCTLAALGASK 587  
554 ILKEMSHLETAEAARATREA---KYERIALDLFSECYSNSRPARFALLVRNRCSWTKC 611  
588 LLKTLAKVNDINAAGESEELANEYETRAVELTECYSSDBDLAEQLLVYSCWAGGSGNC 647  
612 LHLATEADAKAFADHDGVAQFLTRIMWCDMAAGTPIRLLLGAPLCPALVYTNLTFSSEA 671  
648 LELAVEATDQHFIAQPGVQNFSLKOWYGBISRDTKNWKIILCLFIPLVGGGFSFRKK- 706  
672 PLRTGLEDLQDLSDTEKSPLYGLQSRVSELVEAPRAQGRGPRVFLTRWRKFWGAP 731  
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732 VTVFLGNVMYFAFLFTYVLLVDRPPGPGPEVTLVFWFTLVLEIRQGFYDE 791  
726 FVFPSEWNVFYIAFLLLFAYVLLMDHFSVPH---PPELVLYSLVFLVFCDEVQRQWYNGV 782  
792 DTHLVKFTLVGNMKNKDMVAFLFTVGVTCBM---LPSAFBAGRTVLAMDWFVFTLR 848  
783 N-----YFTDLWNVMDTLGLFYIAGIVFRILHSSNKSLSYSGRVIFCLDYIIFTLR 833  
849 LIHIFAIHKQLGPKIIVVERMMKDVFFFLFSLVNLVAYGVTYQALLPHDGRLEWIFPR 908  
834 LIHIFTVSRNLGPKIIMLQRMILIDVFFFLFAXMMVAFVARQGLLRQNRWRIFRS 893  
909 VLYRPLYQIFQIPLDEIDEAR---VNCS-----THPLLE-DSFSCPSLYANMLVILL 959  
894 VYBFLAMFGQVPSD-VDGTYYDFAHCTFTGNESKPLCVLDBEHLNLR-PFEWITPLV 951  
960 VTFLLVNTLLMNLILAMFSYTFQVQGNADMFWKFORYNLIVEHERPALAPPFILLSH 1019  
952 CIYMLSTNILLVNLVAMFGTVGTVQNNQVQWKFQYFLVQVYCSRLNIPFFPIVAY 1011  
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1012 FYMVVKKCFKCCCKEKNMSESSVCCFKNEDNETLAWEGVMKENYLVKINTKANDT-SEEMR 1070  
1080 KTAHRVDFIAXYLG-LRQEKRIK 1103  
1071 HRFQLDTKLDLRLKGLLKEIANKIK 1095

RESULT 7  
US-08-623-679-9  
; Sequence 9, Application US/08623679  
; Patent No. 5674739  
; GENERAL INFORMATION:  
; APPLICANT: Shyjan, Andrew W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; ; DIAGNOSIS, PREVENTION AND TREATMENT OF TUMOR

TITLE OF INVENTION: PROGRESSION  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/623,679  
FILING DATE: 29-MAR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/412,431  
FILING DATE: 29-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07334/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1533 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-623-679-9  
Query Match 20.4%; Score 1240.5; DB 1; Length 1533;  
Best Local Similarity 28.0%; Pred. No. 5.3e-112;  
Matches 357; Conservative 230; Mismatches 449; Indels 241; Gaps 38;  
Qy 40 FVRVPSGVAPSVLFDLLAEWHLPAPNLVSVLVEEQPFAMKSWLRDLVRLKGLVCAOQT 99  
Db 2 YIRVSYDTKPSDLLHVMKQWQLEPKLLISVHGLQNFQMPKLLKQVFGGLIKAAMTT 61  
Qy 100 GAWILTALRVGLARHVQAVRDHSLASTKRVAVAGMASLGRVLHRRILEEAQEDF- 158  
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Qy 159 ---PVHYPEDDGGQGLCSLDSNLSHFIVPEPPGPKGDLTEIRLRLKXHISEQ---- 211  
Db 112 GKDVTRVVQTMNSPLSKLSVLNNSHTHFILADNGLTKYGAEVKLRLLKXHSIQKINT 171  
Qy 212 RAGYGGTGSITFVLCILVNGDPNLTLEIRISRAVEQAAPMLLV---GSGIADVLA----- 264  
Db 172 RLQGG-----VPLVGLVVEGGPNVSVILEYLOEPPIPVVICDGRASDIILSFAHKY 225  
Qy 265 ----ALVNQ---PHLLVPKVAEQKFKBKFPSKHSFWSWEDIVRWTKLQNTSHQHLITVYD 317  
Db 226 CEEGGIINESLREQLLV---TIQKTFNKNKAQSHQLFALIMCEMK-----KXELVTVFR 276  
Qy 318 FEQEGSELDVTILKALVKACKSHSQBPQDYLDELKLAAMDVRDIAKSEIFNGDVW-- 375  
Db 277 MGSEGGQDIEMAILTALLKG---TNVSAP---DQLSALAMNRVDIRSQIFVFGPHWTP 330  
Qy 376 -----KSCD----- 379  
Db 331 LGS LAPPTDSKATEKEKPPMATTKGRGKGGKGGKGVKEVEEETDPKRIELNWNVA 390  
Qy 380 LEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYSRVSRSKSLFLDLQKQEEA 439  
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QY 485 GRP-----GDRRAEKGPAKPTGQKWLLDLN-----QKSENPRDLFLWAVLQNR 530
Db 495 KRPKALKLGMEDDEPPAKGKKKKKKKEEIDIDVDDPAVSRFOYPPHELMVWAVLMKR 554
QY 531 HEMATYFWAMGOEGVAAALAAACKILKEMGHLETEABEA-----RATREAKYERLALDLF 584
Db 555 QKMAVFLWQGEESMAKALVACKLYKAMAHESSESIDLVDISQDLNNSKDFQALALELL 614
QY 585 SECYSNSERAFALLVRRNRCSKTTCLHLATEADAKAFPAHDGVQAFTRIMWG--DMA 642
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QY 874 FFELFSLVNLVAYGVTTQALLPHDGRLEW--IFRRVLRYPLVLIQIFGQIPLDEIDEARVN 932
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QY 980 YTFQVQGNADFWKFORNLVVEHERPALAPPTILLSHLSLTVRRV---PKKAEHKKR 1036
Db 1007 NTFFEVKISNQWKFQRYQLIMTHDRVLPVPPMILLSHIYIIIRLSGRCKRKREGDQ 1066
QY 1037 EHLERDL-----PDPLDQKWTWETVQKENFLSKWEKRRRDEGEVLRKTAHRVDIFAKY 1091
Db 1067 EBRDRGLKLFDSLEELKRLHEEEQCVQHPREK--EDEQSSSDEIRVTSERVENMSMR 1125
QY 1092 LGLLEQEK-----RIKLESQINYCSVLVSSVADV---LAQGGPRSSQHCQ 1136
Db 1126 LBEINERETFMKTSLSQTVDLRLAQLAELSNNRMVNALENLAGIDRSDLIQARS--RASSEC- 1183
QY 1137 EGSQVAADHRGGLDQW 1153
Db 1184 EATYLLROSSINSADGY 1200
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## RESULT 8

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US-08-933-774-9
; Sequence 9, Application US/08933774A
; Patent No. 6025137
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
; FILE REFERENCE: 07334/004003
; CURRENT APPLICATION NUMBER: US/08/933,774A
; CURRENT FILING DATE: 1997-09-19
; EARLIER APPLICATION NUMBER: US 08/623,679
; EARLIER FILING DATE: 1996-03-29
; EARLIER APPLICATION NUMBER: US 08/412,431
; EARLIER FILING DATE: 1995-03-29
; NUMBER OF SEQ ID NOS: 10
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-933-774-9
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Query Match 20.4%; Score 1240.5; DB 3; Length 1533;
Best Local Similarity 28.0%; Pred.No.5.3e-112; Indels 241; Gaps 38;
Matches 357; Conservative 230; Mismatches 449;
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QY 159 ---PVHYPEDDGGSCQPLCSLDSNLSHFTLVPBPGPKGDLGTELRLEKHISEQ---- 211
Db 112 GKDVTRVYQTMGNPLSKLSVLNNSHTHFLAONGTLGKYGAEVKLRRLLEKHISLOKINT 171
QY 212 RAGYGTGSIETPVLCLLVNGDENTLERISRAVEQAAPWLILV--GSGGIADVLA----- 264
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QY 265 ----ALVNO---PHLLVPKVAEKQKEKPPSKHFSWEDIVRMTKLLQNTSHQHLITVYD 317
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QY 318 PEQEGSEELDTVILKALKACKSHSQEPDYLDELKLAVADRVDIKASEIENGDEVW-- 375
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QY 376 -----KSCD----- 379
Db 331 LGS LAPPTDSKATEKEKPPMATTKGGRGKGKGGKVKVEEVEETDPRKIENLNNVNA 390
QY 380 LEEVMDALVSNKPEFVRLFVNDGADVADFLTYGBLOELYRVSRSKSLDFDLQKQBEA 439
Db 391 LEQAMLDALVDRVDFVLLIENGVMQHFITIPRLEELYNTRLGPPTLHLLVRDVKKS 450
QY 440 RUTLAGLGTQQAAREPPAGPAPF--SLHEVSRVLKDFLODACR-----GFYQD 484
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QY 485 GRP-----GDRRAEKGPAKPTGQKWLLDLN-----QKSENPRDLFLWAVLQNR 530
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QY 531 HEMATYFWAMGOEGVAAALAAACKILKEMSHLETEABEA-----RATREAKYERLALDLF 584
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QY 585 SECYSNSERAFALLVRRNRCSKTTCLHLATEADAKAFPAHDGVQAFTRIMWG--DMA 642
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QY 643 AGTPILRLGALPCALVYTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEE 702
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QY 703 L---VEAPRAQGD-----RGPRAVFLTRWRKFWGAPVTVFLGNVVMYFAFLFETYVLL 754
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QY 755 VDFRPPPGPSGEVTLVFWVFTLVLEIRQGFDTDETHLVKKFTLYYVDNWKCDMVA 814
Db 781 VRM---DGWPSLQEWIVISYIVSLALEKIRE--ILMSEPGKLSQKIKVWLYQEWYNIITDLVA 836
QY 815 IFLFIVGVTCTMLPSAFEAF--GRTVLAMDPMVFTLRILHIFAIHKQLGPKIIVVERMKDV 873
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 QY 1137 EGSOLVAADHRGGLDGM 1153  
 Db 1184 EATYLLROSSINSADGY 1200  
 RESULT 9  
 US-09-181-030-9  
 ; Sequence 9, Application US/09181030  
 ; Patent No. 6251597  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shvjan, Andrew W.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION  
 ; TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION  
 ; FILE REFERENCE: 07334/004005  
 ; CURRENT APPLICATION NUMBER: US/09/181,030  
 ; CURRENT FILING DATE: 1998-10-27  
 ; EARLIER APPLICATION NUMBER: US 08/862,442  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: US 08/623,679  
 ; EARLIER FILING DATE: 1996-03-29  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 1533  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-181-030-9

Query Match 20.4%; Score 1240.5; DB 3; Length 1533;  
 Best Local Similarity 28.0%; Pred. No. 5.3e-112;  
 Matches 357; Conservative 230; Mismatches 449; Indels 241; Gaps 38;  
 QY 40 FVRVPSGVAPSVLFDLLAEHLAPNIVSVLVBEEQPFAMKSMIRVLRKGLVKAQST 99  
 Db 2 YIRVSYDKPSSLLHLMVKDQWOLEPCLLSVHGGLQNFEMQPKLQVFGKGLIKAAMTT 61  
 QY 100 GAWILTSALRGLABHVQAVPDHSLASTSKTVRVVVGMAISGLGHLHRLLEEAQEDF- 158  
 Db 62 GAWITGVGVSTGVISHVGDALKDH---SKSRGRVCAIGIAPWGV-----ENKEDLV 111  
 QY 159 ---PVHYPEDDGGSCPLCSLDSNLSHFTLVEPPGPGKDGGLTELRLEKHXISBQ----- 211  
 Db 112 GKDVTRVYQTMSPNPLSKLSVNNSTHTFLADNGTLGKYGAEVKRLRLLEKHXISLQKINT 171  
 QY 212 RAGYGGTGSIEIPVLCILVNGDPNPTLERISRAVEQAAPWLILV---GSGGIADVLA----- 264  
 Db 172 RLQGC-----VPLVGLVVEGGPNVSVIVLEIQBEPTPVVICDGSGRASDILSFAHKY 225  
 QY 265 ----ALVNO---PHLLVPKVAEKQKPEKPPSKHPSWEDIVRWTKLQNTSHOHLITVYD 317  
 Db 226 CEEGIIINESLREQLLV---TIQRTFNYNKAQSHQLFAIMECK-----KKELVTVFR 276

QY 318 FEQGSBELDTVILKALVKACKSHSQBPQDYLDELKLAVAMRDVDAKSIFFNGDVMW-- 375  
 Db 277 MGSEGGQDIEMAILTALLKG--TNVSAP-----DQLSLAAMNRVDIARSOIFVPGHWTP 330  
 QY 376 -----KSCD----- 379  
 Db 331 LGSILAPPTDSKATEKEKPPMATTKGGRGKGGKKGKVEVEFEETDPRIKIELLNWNA 390  
 QY 380 LEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYSYRSRKSLLPDLLOKOEBA 439  
 Db 391 LEQAMLDAVDRVDVFKLLIENGVMQHFLLTPLEELNTRLPNTLHLLVDRVVKKS 450  
 QY 440 RLTIAGLGTQAREPPAGPPAF--SLHEVSRVLKDFLODACC-----GRYQD 484  
 Db 451 NL-----PPDYHISLIDIGLVLEVMGAYRCNRYTRKNFRTLYNNLFGP 494  
 QY 485 GRP-----GDRRAEKGPAPKPTQCKWLLDLN-----QKSENWRDLFLWAVLQNR 530  
 Db 495 KRPKALKLQWEDDEPPAKGKKKKKBEIDIDVDDPAVSRFQYFPHLMWAVLMKR 554  
 QY 531 HEMATYFWMGQEGVAAALAAACKILKEMSHLETEAEAA-----RATREAKYERIALDLF 584  
 Db 555 QKAVFLWQGEESMAKALVACKLYKAMAHESSEDLVDDISQDLNNSKDFGQLALELL 614  
 QY 585 SECYSNSEARAFALLVRRNRCWKTCTCLHLATEADAKAFAHDGQVQAFLTRIWWG--DMA 642  
 Db 615 DQSYKHDEQIATMKLLTYELKNWSNSTCLKLAFAAKHRDFAHTCSQMLLTDMNMLRLMR 674  
 QY 643 AGTIFILLGAFCLPALVYNNLITFSEAPLRTGLEDLQDLSDLTSEKSPLYGQSRVEE 702  
 Db 675 KNPGLKVMIGILLPPTILFLEFRY-----DDFSYQTSKENEDGKEKEEN 720  
 QY 703 L---VEAPRAQGD-----RGPRAVFLLRWRKFGAPVTVFLGNVMVYFAFLFTFYVLL 754  
 Db 721 TDANADAGSRKGDENEHKKQBSIPIGTKICEFYNAPIVKFWFYTISLVGYLLLFNYVIL 780  
 QY 755 VDRPPPPGSGPBVTLYFVWVTLVLEIRQGFDTDETHLVKFTLYVGNWNKCDMVA 814  
 Db 781 VRM---DGWPSLQEWIVISYIVSLALEKIRE-ILMSPPGKLSQKIKVWLQEQYMNITDLVA 836  
 QY 815 IFLFIVGVTCTMLPSAPEA-GRTVLAMDPMVFTLRLLHIFAIHKOLGPKIIVVERMKDV 873  
 Db 837 ISTFMIGAILRLQNPQYMGGRVYICVDIIFWYIRVLDIFGVNKLPGYVMMIGKMMIDM 896  
 QY 874 PFFLFLSVMLVAVGVTQTALLPHDGRLEW-IFRRVLYRPLYQIFGOIPLDEIDEARVN 932  
 Db 897 LYFVVMVLMVMSFGVARQAILHPEE-KPSWKALRNIFYPMYMIYGEVFADQID----- 950  
 QY 933 CSTHPLLEDSPSC-----PSLYANMLVILLVTFLLVTNVLMLNILLIAMS 979  
 Db 951 ----LYAMEINPPCGENLYDEBKRLPPCIPGAWLTPALMACYLLVANILLVNLIIAVFN 1006  
 QY 980 YTFQVQGNADMFWKFORYNLIYVHERPALAPPFILLSHLSLTLRRV---FKKEAEHR 1036  
 Db 1007 NTFPEVKSINQVWKFORQILMTFHDRLVPLPPPMIILSHIYIIMRLSGCRKREGDQ 1066  
 QY 1037 EHLERDL-----PDLQOKVVTWETVOKENFLSKWEXRRRDESEGLRKTAAHRYDFAKY 1091  
 Db 1067 EERDGLKFLSDEELKRLHEFEQCQVEHFREK-EDBQQSSDERIRVTSEVENMSMR 1125  
 QY 1092 LGGUREQK-----RIKLESQINVCYSLVSVADV-----LAQGGGPRSSQHC 1136  
 Db 1126 LEEINERETFMKTSIQTVDLRLAQLEELSNRMVNALENLAGIDRSDLIQARS-RASSEC- 1183  
 QY 1137 EGSOLVAADHRGGLDGM 1153  
 Db 1184 EATYLLROSSINSADGY 1200

RESULT 10  
 US-09-534-242-9  
 ; Sequence 9, Application US/09534242

[illegible]



451	Db	451	NL-----PPDYHSLIDIGLVBLYLGGVRCVNYTRKFTLYNNLFGP	494
485	Qy	485	GRP-----GDRRRAEKGPARKPTGQKWLLDLN-----QKSENPMWDLFWAVLQNR	530
495	Db	495	KRPKALKLWGEDDEPPAKGKKKKKKKEEEDVDVDPVSRFQYPFHELMVWVLMKR	554
531	Qy	531	HEMATYFWANQGEQVAAALAAACKILKEMSHLETEAEAA-----RATREAKYERLALDLF	584
555	Db	555	QKMAVFLWQGEBSMAKALVACKLYKAWAHESSESDLVDDISQDLNNSKDFGQALAE LL	614
585	Qy	585	SECVSNEARAFALLVRNRNCWSTTCLHLHATEADAKAFPAHDGVQAFLTRIWWG--DMA	642
615	Db	615	DQSYKHDEQIATKMLTYTELKNWSNSTCLKVAVAKHRDFIAHTCSQMLLTDMMWRUMR	674
643	Qy	643	AGTPILRLLAGFLCPALVYTNLITFSEAPLRTGLEDLQDLSDLTDEKSPLYGLQSRVEE	702
675	Db	675	KNPGLKVMIGILLPPTILFLEFRY-----DDFSQTSKENEDGKEEEN	720
703	Qy	703	L---VEAPRQGD-----RGPRAVELLTRRKFWGAPVTVPLGNVVMYFAPFLFTTVLL	754
721	Db	721	TDANADAGSKGGBEENHKQRSIPGTCICEFYNAPIVFKFWFTTISYLGYLLENFVIL	780
755	Qy	755	VDFRPPQSGSGBEVTLFYFWVFTLVLEBIEIRQGFPTDEDTHLVKFTLYVGDNNKCDMVA	814
781	Db	781	VRM---DGWESLQEWIVISIVSLALBKIE--ILMSEPGKLSQKIKWLOEYWNITDLVA	836
815	Qy	815	IFLIFVGVTCRMLPSAFEA--GRTVLAMDPMVFTLRLJHIFAIHKQLGPKIIVVERMMKDV	873
837	Db	837	ISTFMIGAILRLNQPMYGRVYCVDDITFWYIRVLDIFGVNKYLGFYVMMIGKWMIDM	896
874	Qy	874	FFLFLFSLVWLAVGVTTOALLHPHGRLEW--IFRRVLYRPILOIFQOIPLDEIDEARVN	932
897	Db	897	LYFVIMLVMLVMSFGVARQAILHPPEE--KPSWKCLARNIFYPMWMIYGEVADQID----	950
933	Qy	933	CSTHPLLEDSPSC-----PSLYANMLVILLVTFLLVTVNLLMLLLIAMFS	979
951	Db	951	----LYAMEINPCGENLYDEBKRLPCTPGAWLTALMACYLLVANILLVLLIAVFN	1006
980	Qy	980	YTVQVQGNADMFWKFORYNLIVEYHERPALAPPTILLSHLSITLRRV---FKKEAEHKR	1036
1007	Db	1007	NTFPEVKISIGNQWKFORYQLITFHDRPVLPPPMIILSHIYIIMLSGRCKRKREGDQ	1066
1037	Qy	1037	EHLERDI-----PDPLDKVVTWETQKENFLSKWEXRRRDSGEVLRKTAHRVDFTAKY	1091
1067	Db	1067	EEDRGUKFLSDEELKRLHEFEQCVOEHFREK--EDEQQSSSDERIRVTSERYENMSMR	1125
1092	Qy	1092	LGLIREQEK-----RIKLESQINYCVLSVSSVADV---LAQGGGPRSSQHCQ	1136
1126	Db	1126	LEEBINERETFKTSLQTVDLRLAQLLELSNRMVNALENACIDRSDLIQARS-RASSEC-	1183
1137	Qy	1137	EGSQLVAAHRGGIDGW	1153
1184	Db	1184	EATYLLRFQSSINSADGY	1200

RESULT 13

```

US-08-623-679-7
; Sequence 7, Application US/08623679
; Patent No. 5674739
; GENERAL INFORMATION:
; APPLICANT: Shvjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITILE OF INVENTION: DIAGNOSIS, PREVENTION AND TREATMENT OF TUMOR
; TITILE OF INVENTION: PROGRESSION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

```





is Page Blank (uspto)



Brannock  
10/02/2018  
Seq ID 8

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 14, 2004, 00:00:43 ; Search time 73 Seconds  
(without alignments)  
4509.149 Million cell updates/sec

Title: US-10-026-188-8  
Perfect score: 6093  
Sequence: 1 MQDVQGRPGSPGDAEDRRE.....HRGGLDGEQPGAGQPPSDT 1165

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_29Jan04.\*
- 1: Genesep1980s.\*
  - 2: Genesep1990s.\*
  - 3: Genesep2000s.\*
  - 4: Genesep2001s.\*
  - 5: Genesep2002s.\*
  - 6: Genesep2003as.\*
  - 7: Genesep2003bs.\*
  - 8: Genesep2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6093	100.0	1165	4	AAB86162	AAB86162 Human MTR
2	6093	100.0	1165	5	AAM51708	AAM51708 Human TRP
3	6093	100.0	1165	5	ABB83855	ABB83855 Human ltr
4	6034	99.0	1179	4	AAB86165	AAB86165 Human MTR
5	5088.5	83.5	1158	4	AAB86164	AAB86164 Mouse MTR
6	5088.5	83.5	1158	5	ABB83854	ABB83854 Mouse ltr
7	5080.5	83.4	1158	4	AAB86166	AAB86166 Mouse MTR
8	5073	83.3	1157	5	AAM51707	AAM51707 Mouse TRP
9	5008.5	82.2	1164	5	ABB83853	ABB83853 Rat L-TRP
10	4534	74.4	872	4	AAB86163	AAB86163 Human MTR
11	2448.5	40.2	1166	5	ABG61907	ABG61907 Prostate
12	2448.5	40.2	1214	3	AAY95436	AAY95436 Human cal
13	2448.5	40.1	1214	3	AAB20283	AAB20283 Human TRP
14	2412.5	39.6	1129	4	AAB85974	AAB85974 Human T1C
15	2353	38.6	1083	6	ABG72088	ABG72088 Human tra
16	2184.5	35.9	1040	5	AAU82018	AAU82018 Human sec
17	2164	35.5	1016	5	ABG61852	ABG61852 Prostate
18	2039	33.5	1469	6	ABR43185	ABR43185 Human REM
19	2039	33.5	1503	3	AAY92944	AAY92944 Human TRP
20	2039	33.5	1503	3	AAY95439	AAY95439 Human cal
21	2039	33.5	1503	3	AB336865	AB336865 Human put
22	2039	33.5	1503	5	ABB76459	ABB76459 Human lon
23	2039	33.5	1503	5	ABB84544	ABB84544 Human tra
24	2039	33.5	1503	7	ADC47022	ADC47022 Human LTR
25	2039	33.5	1503	7	ADC77685	ADC77685 Human 222

26	2039	33.5	1503	7	ADC83633	ADC83633 LTRPC3-te
27	2023.5	33.2	1507	7	ADC47034	ADC47034 Mouse LTR
28	2011	33.0	1508	7	ADC47024	ADC47024 Rat LTRPC
29	1619	26.6	678	5	AAE20284	AAE20284 Human Trp
30	1605.5	26.3	725	3	AAY95434	AAY95434 Human cal
31	1574.5	25.8	1104	3	AAY95437	AAY95437 Human cal
32	1566.5	25.7	1095	2	AAY00931	AAY00931 Prostate-
33	1566.5	25.7	1095	4	AAM01233	AAM01233 P788P ami
34	1566.5	25.7	1095	4	AAU69878	AAU69878 Human pro
35	1566.5	25.7	1095	4	ABU71769	ABU71769 Prostate
36	1566.5	25.7	1095	5	ABB95338	ABB95338 Human p78
37	1566.5	25.7	1095	6	ABR54450	ABR54450 Prostate
38	1566.5	25.7	1095	7	ADB75597	ADB75597 Prostate
39	1566.5	25.7	1095	7	ADB14228	ADB14228 Human pro
40	1563.5	25.7	1104	5	ABG61818	ABG61818 Prostate
41	1558.5	25.6	1095	4	AAM01234	AAM01234 P788P ami
42	1558.5	25.6	1095	4	AAU69879	AAU69879 Human pro
43	1558.5	25.6	1095	4	ABU71770	ABU71770 Prostate
44	1558.5	25.6	1095	5	ABB95339	ABB95339 Human p78
45	1558.5	25.6	1095	6	ABR54451	ABR54451 Prostate

ALIGNMENTS

RESULT 1

AAB86162 AAB86162 standard; protein; 1165 AA.

AC AAB86162;

DT 09-AUG-2001 (first entry)

DE Human MTR1 protein containing exon 18 fragment.

XX MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;  
transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;  
11p15.5 abnormality; chromosome 11; anticancer; developmental activity;  
intracellular calcium ion regulation; hormone; growth factor; apoptosis;  
cell growth; cell death; cell differentiation; urogenital disease;  
polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;  
rhabdomyosarcoma.

OS Homo sapiens.

FN WO200132693-A2.

XX 10-MAY-2001.

PD 06-NOV-2000; 2000WO-DE003876.

PF 04-NOV-1999; 99DE-01053167.

PR (UYGU-) UNIV GUTENBERG JOHANNES.

PA Prawitt D, Pelletier J, Zabel B;

XX WPI; 2001-316417/33.

DR N-PSDB; AAH20574.

XX DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann syndrome and tumors, also related proteins and antibodies.

PT Claim 10; Fig 4; 46pp; German.

CC This invention describes a novel DNA sequence (I) encoding the MTR1 protein that: (i) has at least one biological activity of a TRP (transient receptor potential) family protein; (ii) is connected with etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected with tumors involving 11p15.5 abnormalities. The products of the invention have anticancer and developmental activity. MTR1 is involved in regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis

CC and cell growth, death and differentiation, and in urogenital diseases,  
 CC including polycystic kidney disease. (I) and related ribozymes, antisense  
 CC RNA, proteins and antibodies (Ab)) are used to treat or prevent diseases  
 CC associated with altered expression of the MTR1 gene or activity of its  
 CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,  
 CC thalidomide tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also  
 CC used for diagnosis of such diseases. (I) can also be used for recombinant  
 CC production of MTR1 proteins (II) (used for analysis, characterization and  
 CC therapy), as tissue or chromosomal markers, for identifying genetic  
 CC diseases and related sequences, as primers for genetic fingerprinting, as  
 CC source of oligonucleotides for biochips, and to raise anti-protein or  
 CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in  
 CC competitive assays for (II), as tissue markers, for identifying  
 CC interacting proteins and in screening for (ant)agonists. This sequence  
 CC represents a human MTR1 protein described in the method of the invention  
 XX

SQ Sequence 1165 AA;

Query Match 100.0%; Score 6093; DB 4; Length 1165;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQDVQGRPGSGDAEDRRLGLHRGEVNFEGSGKKGKGFVRVPSGVAPSVLFDLLAAEW 60  
 Db 1 MQDVQGRPGSGDAEDRRLGLHRGEVNFEGSGKKGKGFVRVPSGVAPSVLFDLLAAEW 60

QY 61 HLPAPNLVVSIVGEEQPFAMKSMRLDVLRLKGLVKAAGSTGAWILTSALRVGLARHVQAV 120  
 Db 61 HLPAPNLVVSIVGEEQPFAMKSMRLDVLRLKGLVKAAGSTGAWILTSALRVGLARHVQAV 120

QY 121 RDSLSASTSKRVVAVGMSLGRVLHRRILIEEAQEDFPVHPEDDGGSGQPLCSLDSNL 180  
 Db 121 RDSLSASTSKRVVAVGMSLGRVLHRRILIEEAQEDFPVHPEDDGGSGQPLCSLDSNL 180

QY 181 SHFLLVPEPGKGDGLTELRRLRLKXHSIQRAGYGGTGSIEIPVLCILVNGDPTLIERI 240  
 Db 181 SHFLLVPEPGKGDGLTELRRLRLKXHSIQRAGYGGTGSIEIPVLCILVNGDPTLIERI 240

QY 241 SRVQEAAPWMLILVSGSGIADVLAALVNQPHLLVPKVAEQKFKEKFPKHSWEDIVRWT 300  
 Db 241 SRVQEAAPWMLILVSGSGIADVLAALVNQPHLLVPKVAEQKFKEKFPKHSWEDIVRWT 300

QY 301 KLLQNITSHQHLITVYDFEGSGSELDITVILKALVKAACKSHSQBPQDYLDLKLAVAWDR 360  
 Db 301 KLLQNITSHQHLITVYDFEGSGSELDITVILKALVKAACKSHSQBPQDYLDLKLAVAWDR 360

QY 361 VDIATKSIENGDNVWKSCDLEEVMDVLSNKPFEVRLFDVNGADVADFLTYGLQLYL 420  
 Db 361 VDIATKSIENGDNVWKSCDLEEVMDVLSNKPFEVRLFDVNGADVADFLTYGLQLYL 420

QY 421 SVSRKSLLDLQRLQKQEARLTLAGLGTQQAAREPPAGPAPFSLHEVSRVLKDFLQDACRG 480  
 Db 421 SVSRKSLLDLQRLQKQEARLTLAGLGTQQAAREPPAGPAPFSLHEVSRVLKDFLQDACRG 480

QY 481 FYQGRGDRRRRAEKPAKPTGQKWLDDLNQKSENWRDPLFWAVLQNRHEMATYFWAM 540  
 Db 481 FYQGRGDRRRRAEKPAKPTGQKWLDDLNQKSENWRDPLFWAVLQNRHEMATYFWAM 540

QY 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLSECVSNSEARAFALLV 600  
 Db 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLSECVSNSEARAFALLV 600

QY 601 RRNRCSWKTTCIHLATEADAKAFPAHDGVQAFRLRIWMDGMAAGTPIRLILGAFCLPALV 660  
 Db 601 RRNRCSWKTTCIHLATEADAKAFPAHDGVQAFRLRIWMDGMAAGTPIRLILGAFCLPALV 660

QY 661 YTNLITSEAPRLTGLDLQDLSLDTKSPHGLQSRVDELVEAPRAQDGRGRAVFL 720  
 Db 661 YTNLITSEAPRLTGLDLQDLSLDTKSPHGLQSRVDELVEAPRAQDGRGRAVFL 720

QY 721 LTRWRKFWGAPVTYFLGNVVMYAFLEFLFTTVLLVDFRPPQPGSGPEVTLYFWVFTLV 780  
 Db 721 LTRWRKFWGAPVTYFLGNVVMYAFLEFLFTTVLLVDFRPPQPGSGPEVTLYFWVFTLV 780

QY 781 EETROGFFTDDETHLVKFKFTLYVGDNNWNCMDVAIFLFIYGVTCRMLPSAFEAGRTVLAM 840  
 Db 781 EETROGFFTDDETHLVKFKFTLYVGDNNWNCMDVAIFLFIYGVTCRMLPSAFEAGRTVLAM 840

QY 841 DMVFTLRLLIHFIAHKQLGPKIIVVERMMKDVFFLFFLSVLMVAYGVTTQALLHPHDG 900  
 Db 841 DMVFTLRLLIHFIAHKQLGPKIIVVERMMKDVFFLFFLSVLMVAYGVTTQALLHPHDG 900

QY 901 RLEWIFRRVLYRYLOIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLV 960  
 Db 901 RLEWIFRRVLYRYLOIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLV 960

QY 961 TFLLVNTVLLMNLIIAMFSYTFVOVQGNADMFWKFORYNLIYVHERPALAPPFILLSHL 1020  
 Db 961 TFLLVNTVLLMNLIIAMFSYTFVOVQGNADMFWKFORYNLIYVHERPALAPPFILLSHL 1020

QY 1021 SLTLRRVFKKEAEHKEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEH 1080  
 Db 1021 SLTLRRVFKKEAEHKEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEHLEH 1080

QY 1081 TAHRVDFIAKYLGLREOEKRIKLESQINYSVLVSSVADVLAAQGGPRSSQHCGEQSQ 1140  
 Db 1081 TAHRVDFIAKYLGLREOEKRIKLESQINYSVLVSSVADVLAAQGGPRSSQHCGEQSQ 1140

QY 1141 LVAADHRGGLDGWEQPGAGQPPSDT 1165  
 Db 1141 LVAADHRGGLDGWEQPGAGQPPSDT 1165

RESULT 2  
 AAMS1708  
 ID AAMS1708 standard; protein; 1165 AA.  
 XX AAMS1708;  
 AC AAMS1708;  
 XX 16-JAN-2002 (first entry)  
 DT Human TRP8.  
 DE Mouse; human; TRP8; transient receptor potential channel;  
 KW taste receptor cell; bitter; sweet; flavour enhancer; food; beverage;  
 KW pharmaceutical.  
 XX Homo sapiens.  
 XX OS  
 XX WO200179448-A2.  
 XX 25-OCT-2001.  
 XX 17-APR-2001; 2001WO-US012608.  
 XX 17-APR-2000; 2000US-0197491P.  
 XX 13-APR-2001; 2001US-00834792.  
 XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
 XX Margolskee RF, Huang L, Rong M, Max M, Perez CA;  
 PI WPI; 2002-017608/02.  
 XX N-PSDB; AAI99708.  
 XX A new transient receptor potential channel, designated TRP8, is expressed  
 FT in taste receptor cells and associated with perception of bitter and  
 FT sweet taste, and is useful to find new flavor enhancers.  
 XX Claim 9; Fig 4; 55pp; English.  
 PS The invention relates to a mouse and human transient receptor potential  
 CC channel, TRP8, expressed in taste receptor cells and associated with the  
 CC perception of bitter and sweet taste. Modulators of TRP8 are useful as  
 CC flavour enhancers in foods, beverages and pharmaceuticals  
 XX



Query Match		100.0%; Score 6093; DB 5; Length 1165;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 1165; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MDVQGPSPGDAEDRRLGLHRENVFGSGKRGKFRVPSGVAPSVLPDLLLAEW	60
Db	1	MDVQGPSPGDAEDRRLGLHRENVFGSGKRGKFRVPSGVAPSVLPDLLLAEW	60
Qy	61	HLAPNLVSVLGEOPFAMKSWLRDLVRKGLVKAOSTGAWILTSALRVLARHVGQAV	120
Db	61	HLAPNLVSVLGEOPFAMKSWLRDLVRKGLVKAOSTGAWILTSALRVLARHVGQAV	120
Qy	121	RDHSLASTSTKRVVAVGMSLGRVLRHRRILEEAQEDFPVHYPRDDGSGQSPCLSDSNL	180
Db	121	RDHSLASTSTKRVVAVGMSLGRVLRHRRILEEAQEDFPVHYPRDDGSGQSPCLSDSNL	180
Qy	181	SHFVLVSPGPKGGTGLTELRLEKHISEORAGYGGTGSIEIPVLCVLVNGDPTLRI	240
Db	181	SHFVLVSPGPKGGTGLTELRLEKHISEORAGYGGTGSIEIPVLCVLVNGDPTLRI	240
Qy	241	SRVQQAAPMLILVSGSGIADVALVNOPHLLVPKVAEKOFKEKFSKHSWEDIVRWT	300
Db	241	SRVQQAAPMLILVSGSGIADVALVNOPHLLVPKVAEKOFKEKFSKHSWEDIVRWT	300
Qy	301	KLLQNTSHQHLITVDFEQSGSELDITVILKLVKACKSHSQBPQDYLDLKLAVADR	360
Db	301	KLLQNTSHQHLITVDFEQSGSELDITVILKLVKACKSHSQBPQDYLDLKLAVADR	360
Qy	361	VDIAKSEIFNGDVWZKSCDLBEVMDALVSNKPEFVRLVDNGADVADFLTYGRLOELR	420
Db	361	VDIAKSEIFNGDVWZKSCDLBEVMDALVSNKPEFVRLVDNGADVADFLTYGRLOELR	420
Qy	421	SVSRSKLLFDLLOKQEBEARITLAGLGTQOAREPPAGPPAPSLHEVSRLVLDLQDACRG	480
Db	421	SVSRSKLLFDLLOKQEBEARITLAGLGTQOAREPPAGPPAPSLHEVSRLVLDLQDACRG	480
Qy	481	FYQDGRPGDRRAEKGPAKRTGQKWLDDLNKSNPWRDLFLMAVLQNRHEMATYFWAM	540
Db	481	FYQDGRPGDRRAEKGPAKRTGQKWLDDLNKSNPWRDLFLMAVLQNRHEMATYFWAM	540
Qy	541	GOEGVAAALACKILKENSHELEAARATREAKYERLALDLFSECYNSSEARAFALLV	600
Db	541	GOEGVAAALACKILKENSHELEAARATREAKYERLALDLFSECYNSSEARAFALLV	600
Qy	601	RNRCSWKTCHLATEADAKFAHGVQAFPLTRIMWGDMAAGTPILRLGAFICPALV	660
Db	601	RNRCSWKTCHLATEADAKFAHGVQAFPLTRIMWGDMAAGTPILRLGAFICPALV	660
Qy	661	YTNLITPSEAPLRTGLDQLDLSLDEKSPLYGLQSRVLELVEAPRAQDGRGPRAVFL	720
Db	661	YTNLITPSEAPLRTGLDQLDLSLDEKSPLYGLQSRVLELVEAPRAQDGRGPRAVFL	720
Qy	721	LTRWRKFGAPVTYFLGNVVMYPAFLFTYVLLVDFRPPPGSGPEVTLFWFTVLV	780
Db	721	LTRWRKFGAPVTYFLGNVVMYPAFLFTYVLLVDFRPPPGSGPEVTLFWFTVLV	780
Qy	781	BEIROGFFDETHLVKFKFTLVGNWNKCDMVAIFLTVGVTCRMLPSAFAEAGRTVLAM	840
Db	781	BEIROGFFDETHLVKFKFTLVGNWNKCDMVAIFLTVGVTCRMLPSAFAEAGRTVLAM	840
Qy	841	DMVFTLRLIHTFAIKHQLGPKIIIVVERMKDVFLLPFLSVLVAYGTTQALLHPHDG	900
Db	841	DMVFTLRLIHTFAIKHQLGPKIIIVVERMKDVFLLPFLSVLVAYGTTQALLHPHDG	900
Qy	901	RLFWFRVLYPYLQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLV	960
Db	901	RLFWFRVLYPYLQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLV	960
Qy	961	TELLVTNVLNMLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPFPILLSHL	1020
Db	961	TELLVTNVLNMLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPFPILLSHL	1020
Qy	1021	SUTLRVFKKEAEHKEHLERDLPDLDQKVVTWETVQKENFLSKMEKRRDSEGEVLRK	1080

Db	1021	SUTLRVFKKEAEHKEHLERDLPDLDQKVVTWETVQKENFLSKMEKRRDSEGEVLRK	1080
Qy	1081	TAHRVDFIAKYLGLREOEKRIKLESQINYSVLVSSVADVLAAQGGPRSSQHCGRSQ	1140
Db	1081	TAHRVDFIAKYLGLREOEKRIKLESQINYSVLVSSVADVLAAQGGPRSSQHCGRSQ	1140
Qy	1141	LVAADHRGGLDGWEQPGAGPPSDT	1165
Db	1141	LVAADHRGGLDGWEQPGAGPPSDT	1165

RESULT 4  
AAB86165  
ID AAB86165 standard; protein; 1179 AA.  
XX  
AC AAB86165;  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Human MTR1 protein.  
XX  
KW MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;  
KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;  
KW lip15.5 abnormality; chromosome 11; anticancer; developmental activity;  
KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;  
KW cell growth; cell death; cell differentiation; urogenital disease;  
KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;  
KW rhabdomyosarcoma.  
XX  
OS Homo sapiens.  
XX  
FN WO200132693-A2.  
XX  
PD 10-MAY-2001.  
XX  
PF 06-NOV-2000; 2000WO-DE003876.  
XX  
PR 04-NOV-1999; 99DE-01053167.  
XX  
PA (UYGU-) UNIV GUTENBERG JOHANNES.  
XX  
PI Prawitt D, Pelletier J, Zabel B;  
XX  
DR WPI; 2001-316417/33.  
XX  
PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann  
XX syndrome and tumors, also related proteins and antibodies.  
XX  
PS Disclosure; Fig 12; 46pp; German.  
XX  
CC This invention describes a novel DNA sequence (I) encoding the MTR1  
CC protein that: (i) has at least one biological activity of a TRP  
CC (transient receptor potential) family protein; (ii) is connected with  
CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected  
CC with tumors involving lip15.5 abnormalities. The products of the  
CC invention have anticancer and developmental activity. MTR1 is involved in  
CC regulation of intracellular calcium ion levels, which are essential for  
CC cellular responses to hormones and/or growth factors; also in apoptosis  
CC and cell growth, death and differentiation, and in urogenital diseases,  
CC including polycystic kidney disease. (I) and related ribozymes, antisense  
CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases  
CC associated with altered expression of the MTR1 gene or activity of its  
CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,  
CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also  
CC used for diagnosis of such diseases. (I) can also be used for recombinant  
CC production of MTR1 proteins (II) (used for analysis, characterization and  
CC therapy), as tissue or chromosomal markers, for identifying genetic  
CC diseases and related sequences, as primers for genetic fingerprinting, as  
CC source of oligonucleotides for biochips, and to raise anti-protein or  
CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in  
CC competitive assays for (II), as tissue markers, for identifying  
CC interacting proteins and in screening for (ant)agonists. This sequence

CC represents a human MTR1 protein described in the method of the invention  
 XX Query Match 99.0%; Score 6034; DB 4; Length 1179;  
 SQ Best Local Similarity 98.5%; Pred. No. 0;  
 Sequence 1179 AA; Matches 1162; Conservative 0; Mismatches 2; Indels 16; Gaps 3;

QY 1 MQDVQGPSPGDAEDRRRLGLHGEVNFVGGGKRGKFRVPSGVAPSVLPDLILAWE 60  
 DB 1 MQDVQGPSPGDAEDRRRLGLHGEVNFVGGGKRGKFRVPSGVAPSVLPDLILAWE 60  
 QY 61 HLPAPNLVSLVGEQPFAMKSHLRDLVRKGLVKAQSTGAWILTSALRVGLARHVQAV 120  
 DB 61 HLPAPNLVSLVGEQPFAMKSHLRDLVRKGLVKAQSTGAWILTSALRVGLARHVQAV 120  
 QY 121 RDHSLASTSTKVRVAVGMSLGRVLRHRRILEAQAEDFPVHYPPEDDGGSGPLCSLDSNL 180  
 DB 121 RDHSLASTSTKVRVAVGMSLGRVLRHRRILEAQAEDFPVHYPPEDDGGSGPLCSLDSNL 180  
 QY 181 SHPILVEPPGPGDGLTELRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTLIERI 240  
 DB 181 SHPILVEPPGPGDGLTELRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTLIERI 240  
 QY 241 SRAVEQAAPWLLVVGSGGIADVLAAALVNPQHLVPKVAEKQPKFSPKSHFSDIVRWT 300  
 DB 241 SRAVEQAAPWLLVVGSGGIADVLAAALVNPQHLVPKVAEKQPKFSPKSHFSDIVRWT 300  
 QY 301 KLLQNTITSHQHLITVDFQEGSEELDTVILKALVKACKSHSQEPDYLDELKLAWADR 360  
 DB 301 KLLQNTITSHQHLITVDFQEGSEELDTVILKALVKACKSHSQEPDYLDELKLAWADR 360  
 QY 361 VDIKSEIFNGDVWKSCLDEEVMDVLYSNKPEFVRLFDVNGADVADFLTYGRQLQELR 420  
 DB 361 VDIKSEIFNGDVWKSCLDEEVMDVLYSNKPEFVRLFDVNGADVADFLTYGRQLQELR 420  
 QY 421 SVSRKSLLDLQKQEEARLTLAGITQOAREPPAGPAPFSLHEVSRVLKQFLQACRG 480  
 DB 421 SVSRKSLLDLQKQEEARLTLAGITQOAREPPAGPAPFSLHEVSRVLKQFLQACRG 480  
 QY 481 FYQDGRPGDERRAEKGPAPKPTGOKWLLDLNOKSENPRDLFLWVLQNRHEMATYFWAM 540  
 DB 481 FYQDGRPGDERRAEKGPAPKPTGOKWLLDLNOKSENPRDLFLWVLQNRHEMATYFWAM 540  
 QY 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERIAL-----DLFSECVSNSEARA 595  
 DB 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERIAL-----DLFSECVSNSEARA 595  
 QY 596 FALLVRRNRCSWKTCLHLATADAKAPFAHDGVQAFTRIWMGDMAGTPIILRLGAPL 655  
 DB 601 FALLVRRNRCSWKTCLHLATE-DAKAFFAHDGVQAFTRIWMGDMAGTPIILRLGAPL 659  
 QY 656 CPALVYTNLITFSEAPLRTGLELDQLDLSLDEKSPLYGLOSRLVEELVEAPRAQDRGP 715  
 DB 660 CPALVYTNLITFSEAPLRTGLELDQLDLSLDEKSPLYGLOSRLVEELVEAPRAQDRGP 719  
 QY 716 RAVFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLIVDRPPPPQSGSEVTLTYFW 775  
 DB 720 RAVFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLIVDRPPPPQSGSEVTLTYFW 779  
 QY 776 FTLVLEETROGPTDETHLVKKFTLYVGDNNWKNCDMAIFLFIYGVTCRMLPSFAEGR 835  
 DB 780 FTLVLEETROGPTDETHLVKKFTLYVGDNNWKNCDMAIFLFIYGVTCRMLPSFAEGR 839  
 QY 836 TVLAMDVFWFTLRLTHIFAIHKQLGPKIIVVERMKDVFFFLFLSVMLVAVGVTTQALL 895  
 DB 840 TVLAMDVFWFTLRLTHIFAIHKQLGPKIIVVERMKDVFFFLFLSVMLVAVGVTTQALL 899  
 QY 896 HPDGRLEWIFRVLRYRPLYQIFGQIPLDEIDEARVNCSTHPLLEDGSPCSPLYANMLV 955  
 DB 900 HPDGRLEWIFRVLRYRPLYQIFGQIPLDEIDEARVNCSTHPLLEDGSPCSPLYANMLV 959  
 QY 956 ILLLVTFLLVTVNLLMLLIAMFSYTFQVQGNADMFWKFORNLIIVEYHERPALAPFFI 1015

DB 960 ILLLVTFLLVTVNLLMLLIAMFSYTFQVQGNADMFWKFORNLIIVEYHERPALAPFFI 1019  
 QY 1016 LLSHLSLTLRRVPKKEA-----EHKREHLERDLDPDLQKVVTVETQKFNELSK 1065  
 DB 1020 LLSHLSLTLRRVPKKEA-----EHKREHLERDLDPDLQKVVTVETQKFNELSK 1079  
 QY 1066 MEKRRDSEGEVLKTAHRVDFIAKVLGGIREQEKRIKCLSQINYSVLSSVADVLAQ 1125  
 DB 1080 MEKRRDSEGEVLKTAHRVDFIAKVLGGIREQEKRIKCLSQINYSVLSSVADVLAQ 1139  
 QY 1126 GGGPRSSQHCQEGSQLVAADHRGGLDCWEOPGAGQPPSDT 1165  
 DB 1140 GGGPRSSQHCQEGSQLVAADHRGGLDCWEOPGAGQPPSDT 1179  
 RESULT 5  
 AAB86164  
 ID AAB86164 standard; protein; 1158 AA.  
 XX AAB86164;  
 AC AAB86164;  
 XX 09-AUG-2001 (first entry)  
 DT Mouse MTR1 protein.  
 XX  
 DE MTR1: TRP-related protein; Ca2+ regulation; calcium regulation; tumor;  
 XX transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;  
 XX lip15.5 abnormality; chromosome 11; anticancer; developmental activity;  
 KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;  
 KW cell growth; cell death; cell differentiation; urogenital disease;  
 KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;  
 KW rhabdomyosarcoma.  
 XX  
 OS Mus sp.  
 XX WO200132693-A2.  
 PN 10-MAY-2001.  
 XX 06-NOV-2000; 2000MO-DE003876.  
 XX 04-NOV-1999; 99DE-01053167.  
 XX (UYGU-) UNIV GUTENBERG JOHANNES.  
 PA Prawitt D, Pelletier J, Zabel B;  
 PI WPI; 2001-316417/33.  
 XX N-PSDB; AAH20623.  
 XX  
 PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann  
 PT syndrome and tumors, also related proteins and antibodies.  
 XX  
 PS Disclosure; Fig 11; 46pp; German.  
 XX  
 CC This invention describes a novel DNA sequence (I) encoding the MTR1  
 CC protein that: (i) has at least one biological activity of a TRP  
 CC (transient receptor potential) family protein; (ii) is connected with  
 CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected  
 CC with tumors involving lip15.5 abnormalities. The products of the  
 CC invention have anticancer and developmental activity. MTR1 is involved in  
 CC regulation of intracellular calcium ion levels, which are essential for  
 CC cellular responses to hormones and/or growth factors; also in apoptosis  
 CC and cell growth, death and differentiation, and in urogenital diseases,  
 CC including polycystic kidney disease. (I) and related ribozymes, antisense  
 CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases  
 CC associated with altered expression of the MTR1 gene or activity of its  
 CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,  
 CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also  
 CC used for diagnosis of such diseases. (I) can also be used for recombinant  
 CC production of MTR1 proteins (II) (used for analysis, characterization and  
 CC therapy), as tissue or chromosomal markers, for identifying genetic

CC diseases and related sequences, as primers for genetic fingerprinting, as  
CC source of oligonucleotides for biochips, and to raise anti-protein or  
CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in  
CC competitive assays for (II), as tissue markers; for identifying  
CC interacting proteins and in screening for (ant)agonists. This sequence  
CC represents the murine MTR1 gene described in the method of the invention  
XX  
SQ Sequence 1158 AA;

Query Match 83.5%; Score 5088.5; DB 4; Length 1158;  
Best Local Similarity 84.1%; Pred. No. 0;  
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY 1 MQDVQGRPGSGDAERREGLHGRGVNFGSGKRGKFKVRVSGVAPSVLFDLLAAEW 60  
Db 1 MQTTQSSCGSPPTDEGWEPILCRGHINFGSGKRGKFKVFPSSVAPSVLFDLLAAEW 60  
QY 61 HLPAPNLVSVLGEQPPAMKSWLRDLVRLKGLVKAAGSTGAWILTSALVGLARHVQAV 120  
Db 61 HLPAPNLVSVLGEERPLAMKSWLRDLVRLKGLVKAAGSTGAWILTSALVGLARHVQAV 120  
QY 121 RDHSLASTKVRVAVGMSLGRVLRHRIIE--EAQEDFPVHYVEDDDGGSGPLCSLDS 178  
Db 121 RDHSLASTKVRVAVGMSLGRVLRHRIIE--EAQEDFPVHYVEDDDGGSGPLCSLDS 180  
QY 179 NLSHFILVPEPGPGKG-DGLTELRLRLKHSIEQAGYGGTGSIEIPVLCILVNGDPNTL 237  
Db 181 NLSHFILVESGALSGNDGLTELQSLKHSISQRTGYGGTSCIQIPVLCILVNGDPNTL 240  
QY 238 ERISRAVEQAAPWILVSGSGIADVLAAVNQPHLLVPKVAEKQKFKPSPKHSWEDIV 297  
Db 241 ERISRAVEQAAPWILVSGSGIADVLAAVNQPHLLVPKVAEKQKFKPSPKHSWEDIV 300  
QY 298 RWTKLQNTSHQHLITVYDFEQRSGSELDVTILKALVKACKSHSQEPDQVLDLKLAVA 357  
Db 301 HWTQLQNTSHQHLITVYDFEQRSGSELDVTILKALVKACKSHSQEPDQVLDLKLAVA 360  
QY 358 WDRVDIAKSEIFNGVDEWKSQDEBVMVDALVSNKPEFVRLVFDVNGADVDFLTGRLOE 417  
Db 361 WDRVDIAKSEIFNGVDEWKSQDEBVMVDALVSNKPEFVRLVFDVNGADVDFLTGRLOE 420  
QY 418 LYRSVRSKSLFDLLQKOEABRLTLAGTQQAAREPPAGPPAFSLHEVSRVILKDFLODA 477  
Db 421 LYHSVSPKSLFELLQKHEEGRLLTAGLGAQAARELPGLPAFSLHEVSRVILKDFLODA 480  
QY 478 CRGFYQDG-----RRMEERGPKRPAQKWLPLDLSRSEDPWDLFLWAVLQNRHMAVTF 537  
Db 481 CRGFYQDG-----RRMEERGPKRPAQKWLPLDLSRSEDPWDLFLWAVLQNRHMAVTF 536  
QY 538 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERIALDLFSECYSNSBARAPA 597  
Db 537 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERIALDLFSECYSNSBARAPA 596  
QY 598 LLVRNRCKWTKTCHLATEADAKFAHGDGVAQFLTRIMWGDMAAGTPILLLGAFCLP 657  
Db 597 LLVRNRHNSRTTCHLATEADAKFAHGDGVAQFLTRIMWGDMAAGTPILLLGAFCLP 656  
QY 658 ALVYTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVEELVEAPRAQGRGPRA 717  
Db 657 ALVYTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVEELVEAPRAQGRGPRA 716  
QY 718 VFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDPRPPQSPGSEVTVLYFWVFT 777  
Db 717 VFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDPRPPQSPGSEVTVLYFWVFT 776  
QY 778 LVLEETROQFTDTHLVKKTLYVGNWNNKCDMAIFLFTVGVTCRMLPSAFAGRTV 837  
Db 777 LVLEETROQFTDTHLVKKTLYVGNWNNKCDMAIFLFTVGVTCRMLPSAFAGRTV 836  
QY 838 LAMDEWVFTLRLTHFAIKHQLGPKLIIIVVERWKKDVFFFLFLLSVLWVAYGVTQALLHP 897  
Db 837 LAMDEWVFTLRLTHFAIKHQLGPKLIIIVVERWKKDVFFFLFLLSVLWVAYGVTQALLHP 896

QY 898 HDGRLEWIFRRVLYRPLVLIQIFGOIPLEIDEARVNCSTHPLLEDSPSCPSLVANLVIL 957  
Db 897 HDGRLEWIFRRVLYRPLVLIQIFGOIPLEIDEARVNCSTHPLLEDSPSCPSLVANLVIL 956  
QY 958 LLVTELLVTVLMLNLLIAMFSYTFVQVQGNADMFVKFQRYNLIIVEYHERPALAPPFILL 1017  
Db 957 LLVTELLVTVLMLNLLIAMFSYTFVQVQGNADMFVKFQRYNLIIVEYHERPALAPPFILL 1016  
QY 1018 SHLSLTLRRVFKKEAEHREHLERDLDPDLDQKVVTWETVQKENFLSKMKRRRDSGEV 1077  
Db 1017 SHLSLTLVQLQVFRKEAQHRLERDLDPDLDQKVVTWETVQKENFLSKMKRRRDSGEV 1076  
QY 1078 LRKTAHRVDPIAKYLGRLREQEKRIKLESQINVCVLSGVADVLAAQGGPRSSQHCGE 1137  
Db 1077 LRKTAHRVDPIAKYLGRLREQEKRIKLESQINVCVLSGVADVLAAQGGPRSSQHCGE 1136  
QY 1138 GSQVLAADHRGGLDGEQPGAGQPPSDT 1165  
Db 1137 RSQPASARDREYLE-----SGLPSPDT 1158

RESULT 6  
ABB83854  
ID ABB83854 standard; protein; 1158 AA.  
XX ABB83854;  
XX ABB83854;  
DT 30-SEP-2002 (first entry)  
XX Mouse ltrpc5 SEQ ID NO 5.  
DE Mouse; ltrpc5; taste; cell signalling; TC-ICS; food; pharmaceutical;  
XX taste cell-specific ion channel subunit.  
XX Mus sp.  
XX WO200254069-A1.  
XX 11-JUL-2002.  
XX 26-DEC-2001; 2001WO-US049808.  
XX 29-DEC-2000; 2000US-0259379P.  
XX 21-DEC-2001; 2001US-00026188.  
XX (REGC) UNIV CALIFORNIA.  
XX Zuker CS, Zhang Y;  
XX WPI; 2002-583632/62.  
XX N-PSDB; ABB85734.  
XX Identifying modulators of taste signaling in taste cells for use in food  
XX and pharmaceutical industries to customize and regulate taste, by  
XX determining effect of the compound on a taste cell-specific ion channel  
XX subunit.

Claim 1; Page 211; 306pp; English.  
The invention relates to identifying (M1) a compound that modulates taste  
signalling in taste cells, by contacting the compound with a eukaryotic  
host cell or cell membrane which expresses a taste cell-specific ion  
channel subunit (TC-ICS), and determining a functional effect of the  
compound upon a transmembrane ion flux of a predetermined ion.  
Identifying a compound that modulates taste signalling in taste cells.  
(M1) is useful for identifying a compound that binds to a taste cell  
in taste cells, for identifying a compound that modulates taste signalling  
specific ion channel subunit and for modulating taste signalling by (M1)  
cells of a mammal, in particular a human. Modulators identified by (M1)  
are used by the food and pharmaceutical industries to customize taste,  
e.g. as additives to food or medicine so that the food or medicine tastes  
different to the subject who ingests it. Bitter medicines can be made to  
taste less bitter and sweet substance can be enhanced. The modulators are

CC useful for pharmacological and genetic modulation of taste signalling  
CC pathways. The taste modulators can be directly administered to mammalian  
CC subjects for modulation of taste in vivo. The present sequence is that of  
CC the predicted mouse *ltrpc5* protein of the invention  
XX  
SQ Sequence 1158 AA;

Db	897	HGRLEWIFRRVJYRYPYLIQIFGGIPLDEIDEABVNCSLHPLLLESSACPNLYANMLVIL	956
Qy	958	LLVTFLLVTNVLLMNLIIAMFSYTFVQGNADMFWKFOYNIIVEVHERPALAPPILL	1017
Db	957	LLVTFLLVTNVLLMNLIIAMFSYTFVQGNADMFWKFOYHIIIVEVHERPALAPPILL	1016
Qy	1018	SHLSLTLRRVPFKBAEHRKREHLERDIPDLDQKVTVTWETVQKENFUSKMKRRRDSGEV	1077
Db	1017	SHLSLVLKQVFRKEAQKHQHLERDIPDLDQKIITWETVQKENFISTMKRRRDSGEV	1076
Qy	1078	LRTAHRVDPIAKYLGGLREOEKRIKLESQINVCYSLVSSVADVLAAQGGPPSSQHCGE	1137
Db	1077	LRTAHRVDLIIAKYIGGLREOEKRIKLESQANYCMLLSSMTDTLAPGGTYSSQNCCG	1136
Qy	1138	GSOLVADHRGGLDGWEQPCAGQPPSDT	1165
Db	1137	RSQFASARDREYLE-----SLGPPSDT	1158

## RESULT 7

AAB86166

ID AAB86166 standard; protein; 1158 AA.

XX  
AC AAB86166.

AC  
XX  
DT

XX  
DE Mouse MTR1 protein #2.

XX MTR1, TRP-related protein; Ca2+ regulation; calcium regulation; tumor;  
KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;  
KW 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;  
KW intracellular calcium ion regulation; hormone; growth factor; apoptosis  
KW cell growth; cell death; cell differentiation; urogenital disease;  
KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;  
KW rhabdomyosarcoma.

XX	Mus sp.
OS	

XX  
PN WO200132693-A2.XX  
PD 10-MAY-2001.

06-NOV-2000: 2000WO-DE003876.

XX  
PR 04-NOV-1999; 99DE-01053167.

XX  
PA (UYGU-) UNIV GUTENBERG JOHANNES.

XX  
PI Prawitt D, pelletier J, Zabel B;  
XXXX  
DR WPI; 2001-316417/33.

XX DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann  
PT syndrome and tumors, also related proteins and antibodies.

XX  
PS Disclosure; Fig 12; 46pp; German.

This invention describes a novel DNA sequence (I) encoding the MTR1 protein that: (i) has at least one biological activity of a TRP (transient receptor potential) family protein; (ii) is connected with etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected with tumors involving 11p15.5 abnormalities. The products of the invention have anticancer and developmental activity. MTR1 is involved in regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis and cell growth, death and differentiation, and in urogenital diseases, including polycystic kidney disease. (I) and related ribozymes, antisense RNA, proteins and antibodies (Ab) are used to treat or prevent diseases associated with altered expression of the MTR1 gene or activity of its protein, or with calcium influx into cells, e.g. BWS, Wilms tumor, rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also used for diagnosis of such diseases. (I) can also be used for recombinant



CC production of MTR1 proteins (II) (used for analysis, characterization and  
 CC therapy), as tissue or chromosomal markers, for identifying genetic  
 CC diseases and related sequences, as primers for genetic fingerprinting, as  
 CC source of oligonucleotides for biochips, and to raise anti-protein or  
 CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in  
 CC competitive assays for (II), as tissue markers; for identifying  
 CC interacting proteins and in screening for (ant)agonists. This sequence  
 CC represents the murine MTR1 gene described in the method of the invention  
 XX  
 SQ Sequence 1158 AA;

Query Match 83.4%; Score 5080.5; DB 4; Length 1158;  
 Best Local Similarity 84.0%; Pred. No. 0;  
 Matches 981; Conservative 67; Mismatches 107; Indels 13; Gaps 4;

QY 1 MQDVQPPGPGDAEDRELGLHGEVNFSGSKKGFVRVPSGVAPSVLFOLLIAEW 60  
 DB 1 MQTTQSSCPGSPPTDGEWEPILCRGEINFGSGKGRKFKVFPSSVAPSVLFELLTEW 60  
 QY 61 HLPAPNLVSVLGEOPFAMKSWLRDLVRKGLVAAQSTGAWILTSALRVGLARHVGQAV 120  
 DB 61 HLPAPNLVSVLGEOPFAMKSWLRDLVRKGLVAAQSTGAWILTSALRVGLARHVGQAV 120  
 QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--BAQEDFPVHPEDDGGSGQPLCSLDS 178  
 DB 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--BAQEDFPVHPEDDGGSGQPLCSLDS 180  
 QY 179 NLSHFILVEPPGKGG-DGLTELRLRLKHSIQEQAGYGGTGTSTIPVLCILVNGDPNTL 237  
 DB 181 NLSHFILVESGALSGNDGLTELQLSLEKHSIQRTGYGGTGTSTIPVLCILVNGDPNTL 240  
 QY 238 ERISRAVOAPWLLVSGGGIADVLAALVNOPHLLVPKVAEKQFKPPSKHFSWEDIV 297  
 DB 241 ERISRAVOAPWLLVSGGGIADVLAALVNOPHLLVPKVAEKQFKPPSKHFSWEDIV 300  
 QY 298 RWTKLQNTSHQHLLTYVDFEQGSBELDTVILKALVKACKSHSQEPQDYLDLKLAVA 357  
 DB 301 HWTLLQNTIAAPHLLTYVDFEQGSBELDTVILKALVKACKSHSQEPQDYLDLKLAVA 360  
 QY 358 WDRVDIAKSEIFNGDVEWKSCLDEVMVDALVSNKPEFVRLPVDNGADVADFLTYGRLOE 417  
 DB 361 WDRVDIAKSEIFNGDVEWKSCLDEVMVDALVSNKPEFVRLPVDNGADVADFLTYGRLOE 420  
 QY 418 LYRSVRSKSLFLDLQKQEEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDLQDA 477  
 DB 421 LYHSVSPKSLFLDLQKQEEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDLQDA 480  
 QY 478 CRGFYQDGRPDRRAEAKGPAKPTGQKWLIDLNOKSENPDWDLFLWAVLQNHMATYF 537  
 DB 481 CRGFYQDGRPDRRAEAKGPAKPTGQKWLIDLNOKSENPDWDLFLWAVLQNHMATYF 536  
 QY 538 WAMGREGVAAALAAACKIKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAPA 597  
 DB 537 WAMGREGVAAALAAACKIKEMSHLETEAARATREAKYERLALDLFSECYNSSEARAPA 596  
 QY 598 LLVRRNRCKWTKTCLHLATEADAKAFFAHGQVQAFILRIWGDMAAGTPIRLLLGAFLCP 657  
 DB 597 LLVRRNRCKWTKTCLHLATEADAKAFFAHGQVQAFILRIWGDMAAGTPIRLLLGAFLCP 656  
 QY 658 ALVYTNLTIFSEAPLRTGLELDLQDLSLDTSEKSPYGLQSRVEELVEAPRAGRGPPA 717  
 DB 657 ALVYTNLTIFSEAPLRTGLELDLQDLSLDTSEKSPYGLQSRVEELVEAPRAGRGPPA 716  
 QY 718 VFLLTWRKFWGAPVTVFLGNVMVFAFLFTYLLVDFRPPPGQSPGPEVTLYFWVFT 777  
 DB 717 AFLLTWRKFWGAPVTVFLGNVMVFAFLFTYLLVDFRPPPGQSPGPEVTLYFWVFT 776  
 QY 778 LVLEERIQGFPTDEDTHLVKKTFLYVGDNNKCDMVAIFLVIGVTCRMLPSAFAGRTV 837  
 DB 777 LVLEERIQGFPTDEDTHLVKKTFLYVGDNNKCDMVAIFLVIGVTCRMLPSAFAGRTV 836  
 QY 838 LAMDEWVFTLRLTHI PAHKQLGPKLIIVERMMKDVFFFLFSLVWLVAVGVTQALLHP 897

DB 837 LAIDFMVFTLRLTHI PAHKQLGPKLIIVERMMKDVFFFLFSLVWLVAVGVTQALLHP 896  
 QY 898 HDGRLEWIFRRVLYRPYLQIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVL 957  
 DB 897 HDGRLEWIFRRVLYRPYLQIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVL 956  
 QY 958 LLVTFLLTVNVLNLLIAMFSYTFQVVOGNADMFQWFORNLIVEHSPALAPPFILL 1017  
 DB 957 LLVTFLLTVNVLNLLIAMFSYTFQVVOGNADMFQWFORNLIVEHSPALAPPFILL 1016  
 QY 1018 SHLSLTLRRVFKKEAEHREHLERLDPDLDOKVVTWETVOKENFLSKMEKRRRDSGEV 1077  
 DB 1017 SHLSLTLRRVFKKEAEHREHLERLDPDLDOKVVTWETVOKENFLSKMEKRRRDSGEV 1076  
 QY 1078 LRKTAHRVDLFIATKYLGLREQEKIKCLESQINYSVSVADVLAQGGGPRSSQHCGE 1137  
 DB 1077 LRKTAHRVDLFIATKYLGLREQEKIKCLESQINYSVSVADVLAQGGGPRSSQHCGE 1136  
 QY 1138 GSQILVADHRGGLDGWEQPGAGQPPSDT 1165  
 DB 1137 RSQPASARDREYLE-----SGLPPSDT 1158

## RESULT 8

AAM51707

ID AAM51707 standard; protein; 1157 AA.

XX AAM51707;

XX 16-JAN-2002 (first entry)

XX Mouse TRP8.

XX Mouse; human; TRP8; transient receptor potential channel;

XX taste receptor cell; bitter; sweet; flavour enhancer; food; beverage;

XX pharmaceutical.

XX Mus sp.

XX Key Location/Qualifiers

XX Misc-difference 467

XX /note= "Encoded by CACGAG"

XX WO200179448-A2.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-US012608.

XX 17-APR-2000; 2000US-0197491P.

XX 13-APR-2001; 2001US-00834792.

XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.

XX Margolske RF, Huang L, Rong M, Max M, Perez CA;

XX WPI; 2002-017608/02.

XX N-PSDB; AAI99707.

XX A new transient receptor potential channel, designated TRP8, is expressed  
 XX in taste receptor cells and associated with perception of bitter and  
 XX sweet taste, and is useful to find new flavor enhancers.

XX Claim 8; Fig 2; 55pp; English.

XX The invention relates to a mouse and human transient receptor potential  
 XX channel, TRP8, expressed in taste receptor cells and associated with the  
 XX perception of bitter and sweet taste. Modulators of TRP8 are useful as  
 XX flavour enhancers in foods, beverages and pharmaceuticals

XX Sequence 1157 AA;

Query Match 83.3%; Score 5073; DB 5; Length 1157;



Best Local Similarity 84.0%; Pred. No. 0;		Matches 981; Conservative 67; Mismatches 106; Indels 14; Gaps 5;	
QY	1	MQVQGRPGSPGDAEDRRRLGHRGVNFGGSKRGKFRVPSGVAPSVLPDLILAEW	60
Db	1	MQVQSCPGSPPTDQGWPILCRGINFGGSKRGKFRVPSGVAPSVLPFELLITW	60
QY	61	HLPAPIVLSVGEQPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRGLARHVGOAV	120
Db	61	HLPAPIVLSVGEERPLANKSWLRDLVRKGLVKAAQSTGAWILTSALRGLARHVGOAV	120
QY	121	RHSLASTSTKRVVAVGMSLGRVLRHRRILE--EAQEDFPVHYDPDGGSGPLCLSDS	178
Db	121	RHSLASTSTKIRVVAIGMASLGRILRQLLDGWHQKEDTPIHYPADEGNIQGPLCLDS	180
QY	179	NLSHFILVEPGPGKG-DGLTELRLRLEKHSORAGYGGTGTIEIPVLCLLVNGDNTL	237
Db	181	NLSHFILVESGALGSGNDGTEILQLSLEKHSQRTGYGGTGTICIQIPVLCLLVNGDNTL	240
QY	238	ERISRAVEQAAPMLILVSGGIIADVLAALVNPHELLVPKVAEKQKFKPFSKHSFSDIV	297
Db	241	ERISRAVEQAAPMLILAGSGIADVLAALVNPHELLVPQVAEKQKFKPFSKHSFSDIV	300
QY	298	RWTKLLQNTSHOHLTVYDFEKGSEELDTVILKALVKACKSHSQPQDYLDLKLAVA	357
Db	301	HWTELLQNTAAHPHLLTVYDFEKGSEELDTVILKALVKACKSHSQPQDYLDLKLAVA	360
QY	358	WRVDIAKSEIFNGDVEWKSCLDEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLOE	417
Db	361	WRVDIAKSEIFNGDVEWKSCLDEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLOE	420
QY	418	LYRSVRKSLLLFOLLQKQOEALRTLAGLTQOAREPPAGPPAFSLHEVSRVLKDFLQDA	477
Db	421	LYHSVPKSLLLFOLLQKQOEALRTLAGLTQOAREPPAGPPAFSLHEVSRVLKDFLQDA	479
QY	478	CRGFYQDGRPGRRRAKGPAPKPTQKWLILNOKSENPRDLFWAVLQNRHEMATYF	537
Db	480	CRGFYQDGRPGRRRAKGPAPKPTQKWLILNOKSENPRDLFWAVLQNRHEMATYF	535
QY	538	WAMQGVGAALAAACKILKEMSHLETEAARAATREAKYERLALDFSECYNSSEARAFA	597
Db	536	WAMQGVGAALAAACKILKEMSHLETEAARAATREAKYERLALDFSECYNSSEARAFA	595
QY	598	LLVRNRCKSKTCLHLATEADAKAFHAGDGVQAPLRIWGDMAAGTPIRLLAGFLCP	657
Db	596	LLVRNRCKSKTCLHLATEADAKAFHAGDGVQAPLRIWGDMAAGTPIRLLAGFLCP	655
QY	658	ALVYTNLITFSEAPLRTGLEODLSDLTDEKSPLYGLQSRVEELVEAPRAGGGRPA	717
Db	656	ALVYTNLITFSEAPLRTGLEODLSDLTDEKSPLYGLQSRVEELVEAPRAGGGRPA	715
QY	718	VFLLRWRKFWGAPVTVFLGNVVMVPAFLFTYVLLVDFRPPPGSPGPEVTVLFWVFT	777
Db	716	AFLLLRWRKFWGAPVTVFLGNVVMVPAFLFTYVLLVDFRPPPGSPGPEVTVLFWVFT	775
QY	778	LVLBIROGFFDDETHLVKFTLYVGDNNKCDMVAIFLFIYGVTCRMLPSAFAGRTV	837
Db	776	LVLBIROGFFDDETHLVKFTLYVGDNNKCDMVAIFLFIYGVTCRMLPSAFAGRTV	835
QY	838	LAMDPMVFTLRILHIFAIHQIGPKIIVVERMKDVFFLFLSVLVAIVGTTQALLHP	897
Db	836	LAMDPMVFTLRILHIFAIHQIGPKIIVVERMKDVFFLFLSVLVAIVGTTQALLHP	895
QY	898	HDGRLEWIFRRVLYRPYQIFQIPLDEIDARVNCSTHPLLEDSPSCPSIYANWLVL	957
Db	896	HDGRLEWIFRRVLYRPYQIFQIPLDEIDARVNCSTHPLLEDSPSCPSIYANWLVL	955
QY	958	LLVTELLVNTVLLMNLIIAMFSYTFQVQGNADMEFKFQRYNLIYVYHERPALAPFFILL	1017
Db	956	LLVTELLVNTVLLMNLIIAMFSYTFQVQGNADMEFKFQRYNLIYVYHERPALAPFFILL	1015
QY	1018	SHLSITLRVFKKEAHEKREHLERDLPDLQKVTVTWVQENFLSKMKERRDSEGEV	1077
Db	1016	SHLSITLRVFKKEAHEKREHLERDLPDLQKVTVTWVQENFLSKMKERRDSEGEV	1075
QY	1078	LRKTAHRVDIAKGLRQEKRIKLESQINVCVSVLVSSADVLAQGGGPRSSQCGE	1137
Db	1076	LRKTAHRVDIAKGLRQEKRIKLESQINVCVSVLVSSADVLAQGGGPRSSQCGE	1135
QY	1138	GSQLVAAADHRRGLDGEQPGAGOPPSDT	1165
Db	1136	RSQPASAREYLE-----SGLPPSDT	1157
RESULT 9			
ABB83853			
ID	ABB83853	standard; protein; 1164 AA.	
XX	AC	ABB83853;	
XX	DT	30-SEP-2002 (first entry)	
XX	DE	Rat L-TRP SEQ ID NO 2.	
XX	KW	Rat; L-TRP; taste; cell signalling; TC-ICS; food; pharmaceutical;	
XX	KW	taste cell-specific ion channel subunit.	
XX	OS	Rattus sp.	
XX	PN	WO200254069-A1.	
XX	PD	11-JUL-2002.	
XX	PF	26-DEC-2001; 2001WO-US049808.	
XX	PR	29-DEC-2000; 2000US-0259379P.	
XX	PR	21-DEC-2001; 2001US-00026188.	
XX	PA	(REGC ) UNIV CALIFORNIA.	
XX	PI	Zuker CS, Zhang Y;	
XX	DR	WPI; 2002-583632/62.	
XX	DR	N-PSDB; ABB85732.	
XX	PT	Identifying modulators of taste signaling in taste cells for use in food	
XX	PT	and pharmaceutical industries to customize and regulate taste, by	
XX	PT	determining effect of the compound on a taste cell-specific ion channel	
XX	PS	subunit.	
XX	PS	Claim 1; Page 63; 306pp; English.	
XX	CC	The invention relates to identifying (M1) a compound that modulates taste	
XX	CC	signalling in taste cells, by contacting the compound with a eukaryotic	
XX	CC	host cell or cell membrane which expresses a taste cell-specific ion	
XX	CC	channel subunit (TC-ICS), and determining a functional effect of the	
XX	CC	compound upon a transmembrane ion flux of a predetermined ion,	
XX	CC	identifying a compound that modulates taste signaling in taste cells.	
XX	CC	(M1) is useful for identifying a compound that modulates taste signalling	
XX	CC	in taste cells, for identifying a compound that binds to a taste cell	
XX	CC	specific ion channel subunit and for modulating taste signaling in taste	
XX	CC	cells of a mammal, in particular a human. Modulators identified by (M1)	
XX	CC	are used by the food and pharmaceutical industries to customize taste	
XX	CC	e.g. as additives to food or medicine so that the food or medicine tastes	
XX	CC	different to the subject who ingests it. Bitter medicines can be made to	
XX	CC	taste less bitter and sweet substance can be enhanced. The modulators are	
XX	CC	useful for pharmacological and genetic modulation of taste signalling	
XX	CC	pathways. The taste modulators can be directly administered to mammalian	
XX	CC	subjects for modulation of taste in vivo. The present sequence is that of	
XX	CC	the rat L-TRP protein of the invention	
XX	SQ	Sequence 1164 AA;	
Query Match 82.2%; Score 5008.5; DB 5; Length 1164;			
Best Local Similarity 82.8%; Pred. No. 0;			
Matches 965; Conservative 77; Mismatches 113; Indels 11; Gaps 3;			

Qy	1	MDVQGPFGPGDAEDRRRLGLHGEVNFSGSKKGFVRVPSGVAPSVLPDLILAEW	60
Dd	9	MPMAQSSCPGSPPTDGTGWEVPLCKGEVNFSGSKKGFVKVPSNVAPSMFLFELLITW	68
Qy	61	HLPAFNLVSVLAGEEQFPAKMSWLRDLVRLKGLVKAAQSTGAWILTSALRVGLARHVQAV	120
Dd	69	HLPAFNLVSVLAGEERLPAKMSWLRDLVRLKGLVKAAQSTGAWILTSALRVGLARHVQAV	128
Qy	121	RDHSLASTSTKRVVAVGMAISLGRVLRHRLLEBAQEDPVHYPEDDGGSQPLCSLDSNL	180
Dd	129	RDHSLASTSTKRVVAVGMAISLGRVLRHRLLEBAQEDPVHYPEDDGGSQPLCSLDSNL	188
Qy	181	SHFILTVEPGPKGK-DGTELRRLRLEKHSORAGYGGTGIETPVLCLLVNGDPNTLER	239
Dd	189	SHFILTVEPGTUGSGNDGLAEQLSLEKHSORAGYGGTGIETPVLCLLVNGDPNTLER	248
Qy	240	ISRAVEQAAPWLIILVGGGIIADVLAAALVNOPHLIVPKVAEQKPKFSPKSHFSNEDIVRW	299
Dd	249	MSRAVEQAAPWLIILVGGGIIADVLAAALVNOPHLIVPKVAEQKPKFSPKSHFSNEDIVRW	308
Qy	300	TKLQNTTSHOHLITVDFEGSGEELDTVILKALVKACKSHSQBPQDYLDELKLAUAWD	359
Dd	309	TELLQNTAAHPHLLTVDFEGSGEELDTVILKALVKACKSHSQBPQDYLDELKLAUAWD	368
Qy	360	RVDIAKSIIFNGDVEWKCDEEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELY	419
Dd	369	RVDIAKSIIFNGDVEWKCDEEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELY	428
Qy	420	RSVRSKSLFLLQKQBEARLTLAGLGTQQAAREPPAGPAPFSLHEVSRVLKDFLODACR	479
Dd	429	HSVPSKSLFELLERKEEGRLLTAGLGAQQTAKLPGVLPAPFSLHEVSRVLKDFLODACR	488
Qy	480	GEYQGRGDRRAEKGAKPTGOKWLLDNLKSENKRDLPFLWAVLQNRHETATYFWA	539
Dd	489	GEYQDG----RMEKRGKPKPAGQKWLDPKSKSEDPMDRDLFWAVLQNRHETATYFWA	544
Qy	540	MGQGVAAALAAACKILKMSHLETAEAARAPREAKYERLALDLFSECVSNSEARAFALL	599
Dd	545	MGREGVAAALAAACKILKMSHLEKEAEVARTWEAKYERLALDLFSECVSNSEARAFALL	604
Qy	600	VRNRCSKSTTCLHLATADAKAFPAHGVQAFPLTRIWMGDMAAGTPILRLGAFCLPAL	659
Dd	605	VRNRCSKSTTCLHLATADAKAFPAHGVQAFPLTRIWMGDMAAGTPILRLGAFCLPAL	664
Qy	660	VYTNLITSEAPLATGLEDLQDLSLDEKSPLYGLQSRVEELVEAPRAQDGRPAFV	719
Dd	665	IYTNLITSEAPLATGLEDLQDLSLDEKSPLYGLQSRVEELVEAPRAQDGRPAFV	724
Qy	720	LLTRWRKFGAPVTVFLGNVVMYFAPLFTTYVLLVDFRPPQPGSPGSEVTVLYFWVFTLV	779
Dd	725	LLTRWRKFGAPVTVFLGNVVMYFAPLFTTYVLLVDFRPPQPGSPGSEVTVLYFWVFTLV	784
Qy	780	LBEIRQGPPTDDBTHLVKFTLYVGDNNKNDMAIFLFIIVGTCBMLBSAFAEAGTVLA	839
Dd	785	LBEIRQGPPTDDBTHLVKFTLYVGDNNKNDMAIFLFIIVGTCBMLBSAFAEAGTVLA	844
Qy	840	MDPMVFTLRIHFAHKGOLGPKIIVVERMKDVRPFLEFLSVLWVAYGVTTQALLPHD	899
Dd	845	IDFMVFTLRIHFAHKGOLGPKIIVVERMKDVRPFLEFLSVLWVAYGVTTQALLPHD	904
Qy	900	GRLEWIFRVLRYPLQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVLILL	959
Dd	905	GRLEWIFRVLRYPLQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVLILL	964
Qy	960	VTPLLVNVLNMLLIAMSYFQVQVADMPKQRYNLIYEHYERPALAPPFTLLSH	1019
Dd	965	VTPLLVNVLNMLLIAMSYFQVQVADMPKQRYNLIYEHYERPALAPPFTLLSH	1024
Qy	1020	LSLTLARVFKAEHREHLERLDPDLQKVVTVETVOKENFLSKMKRRRDRSEGEVLR	1079
Dd	1025	LSLTLARVFKAEHREHLERLDPDLQKVVTVETVOKENFLSKMKRRRDRSEGEVLR	1084
Qy	1080	KTARHVDVFIKYLGLREQEKRIKLESQINQSVLVSSVADVLQAGGPPRESSQHCGBGS	1139
Dd	1085	KTARHVDVFIKYLGLREQEKRIKLESQINQSVLVSSVADVLQAGGPPRESSQHCGBGS	1144
Qy	1140	QLVNAADHRGGLDGEWQFQAGQPPSDT	1165
Dd	1145	QPASARDREYDE-----AGLPHSDT	1164
RESULT 10			
AAB86163			
ID	AAB86163 standard; protein; 872 AA.		
XX	AAB86163;		
AC	AC		
XX	09-AUG-2001 (first entry)		
DT	Human MTR1 protein without exon 18 fragment.		
DE	MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;		
XX	transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;		
KW	11p15.5 abnormality; chromosome 11; anticancer; developmental activity;		
KW	intracellular calcium ion regulation; hormone; growth factor; apoptosis;		
KW	cell growth; cell death; cell differentiation; urogenital disease;		
KW	polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;		
KW	rhabdomyosarcoma.		
XX	Homo sapiens.		
OS	WO200132693-A2.		
FN	10-MAY-2001.		
XX	06-NOV-2000; 2000WO-DE003876.		
PF	04-NOV-1999; 99DE-01053167.		
PR	(UYGU-) UNIV GUTENBERG JOHANNES.		
XX	Prawitt D, Pelletier J, Zabel B;		
PA	WPI: 2001-316417/33.		
PI	N-PSDB; AAH20574.		
PI	DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann		
DR	syndrome and tumors, also related proteins and antibodies.		
DR	Claim 10; Fig 4; 46pp; German.		
XX	This invention describes a novel DNA sequence (I) encoding the MTR1		
CC	protein that: (i) has at least one biological activity of a TRP		
CC	(transient receptor potential) family protein; (ii) is connected with		
CC	etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected		
CC	with tumors involving 11p15.5 abnormalities. The products of the		
CC	invention have anticancer and developmental activity. MTR1 is involved in		
CC	regulation of intracellular calcium ion levels, which are essential for		
CC	cellular responses to hormones and/or growth factors; also in apoptosis		
CC	and cell growth, death and differentiation, and in urogenital diseases,		
CC	including polycystic kidney disease. (I) and related ribozymes, antisense		
CC	RNA, proteins and antibodies (Ab) are used to treat or prevent diseases		
CC	associated with altered expression of the MTR1 gene or activity of its		
CC	protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,		
CC	rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also		
CC	used for diagnosis of such diseases. (I) can also be used for recombinant		
CC	production of MTR1 proteins (II) (used for analysis, characterization and		
CC	therapy), as tissue or chromosomal markers, for identifying genetic		
CC	diseases and related sequences, as primers for genetic fingerprinting, as		
CC	source of oligonucleotides for biochips, and to raise anti-protein or		
CC	anti-DNA antibodies. (II) are used to raise Ab, as reagents in		
CC	competitive assays for (II), as tissue markers; for identifying		
CC	interacting proteins and in screening for (ant)agonists. This sequence		
CC	represents a human MTR1 protein described in the method of the invention		

SQ		Sequence 872 AA;	
Query Match		74.4%; Score 4534; DB 4; Length 872;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches		869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MDVQGP	PGSGDADREELGHRGEVNF
DB	1	MDVQGP	PGSGDADREELGHRGEVNF
QY	61	HLPA	NLVSVLGEQPFAMKSWL
DB	61	HLPA	NLVSVLGEQPFAMKSWL
QY	121	RDHSL	ASTSTKRVVAVGASLGRV
DB	121	RDHSL	ASTSTKRVVAVGASLGRV
QY	181	SHFIL	VEPPGKDGGLTELRL
DB	181	SHFIL	VEPPGKDGGLTELRL
QY	241	SRVQ	QAAPWILVSGSGIAD
DB	241	SRVQ	QAAPWILVSGSGIAD
QY	301	KLLQ	NITSHOHLTVYDFE
DB	301	KLLQ	NITSHOHLTVYDFE
QY	361	VDIA	KSEIFNGDVEWKS
DB	361	VDIA	KSEIFNGDVEWKS
QY	421	SVSR	KSLFDLLQKQEAR
DB	421	SVSR	KSLFDLLQKQEAR
QY	481	FYQD	RCPDRRAEKGPA
DB	481	FYQD	RCPDRRAEKGPA
QY	541	QEGV	AAALAAACKILK
DB	541	QEGV	AAALAAACKILK
QY	601	RRNC	WSKTTCHLATE
DB	601	RRNC	WSKTTCHLATE
QY	661	YTNL	ITSEAPLRTGLD
DB	661	YTNL	ITSEAPLRTGLD
QY	721	LTRW	KFWGAPVTFLGN
DB	721	LTRW	KFWGAPVTFLGN
QY	781	BEIQ	GFTDEDDHLV
DB	781	BEIQ	GFTDEDDHLV
QY	841	DMV	FTLRLIHFAI
DB	841	DMV	FTLRLIHFAI
RESULT 11		ABG61907	
ID		ABG61907 standard; protein; 1166 AA.	
XX		AC	
XX		ABG61907;	
XX			
DT		15-AUG-2002 (first entry)	
XX		Prostate cancer-associated protein #108.	
XX		Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.	
XX		Mammalia.	
XX		WO200230268-A2.	
XX		18-APR-2002.	
XX		12-OCT-2001; 2001WO-US032045.	
XX		13-OCT-2000; 2000US-00687576.	
XX		08-DEC-2000; 2000US-00733288.	
XX		08-DEC-2000; 2000US-00733742.	
XX		24-JAN-2001; 2001US-0263957P.	
XX		16-MAR-2001; 2001US-0276791P.	
XX		16-MAR-2001; 2001US-0276888P.	
XX		06-APR-2001; 2001US-0281922P.	
XX		24-APR-2001; 2001US-0286214P.	
XX		30-APR-2001; 2001US-00847046.	
XX		04-MAY-2001; 2001US-0288589P.	
XX		(EOSB-) EOS BIOTECHNOLOGY INC.	
XX		Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;	
XX		WPI: 2002-471335/50.	
XX		N-PSDB; ABK92224.	
XX		Detecting a prostate cancer-associated transcript in a cell in a patient,	
XX		useful for diagnosing prostate cancer (PC) or screening modulators of PC,	
XX		by determining if prostate cancer-associated genes are expressed in a	
XX		prostate tissue.	
XX		Claim 27; Page 391; 436pp; English.	
XX		The present invention relates to methods of detecting a prostate cancer-	
XX		associated transcript in a cell from a patient. The method comprises	
XX		contacting a biological sample from the patient with prostate cancer-	
XX		associated polynucleotides (designated PC genes) that selectively	
XX		hybridise to a sequence that is at least 80% identical to them. The	
XX		prostate cancer-associated polynucleotide sequences are differentially	
XX		expressed in prostate tumour tissue or	

RESULT 11
ABG61907
ID ABG6
XX
AC ABG6
XX



Db 250 RLRLSYISQKTVGGTG-IDIVLILLIDGDEKMLTRIENATQAOLPCLLVAGSGAA 308  
Qy 261 DVLAALVNQPHLLVP-----KVAEKQFKEKPKSFHFWEDIVRWTKLQNTISHQHLL 313  
Db 309 DCLAETLED--TLAPSGGARQGEARDIRFFPK-----GDLEVLQAQVERIMTRKELL 361  
Qy 314 TVYDFEGSGEELDTVLKALVKACKSHSQBPQDYLDELKLAAMDVRDIAKSEIFNGDV 373  
Db 362 TVYSSE-DGSEEFETIVLKVKAC--GSSEASAYLDELRLAVANVRVDIAQSELFRGDI 418  
Qy 374 EWKSCDLEEVWVDALVSNKPEFVRLFDVNGADVADFLTYGLQLYRSVSRKSLFLDLQ 433  
Db 419 QWRSFHLASLMDALLNDREFFVRLISHGLSHGFLTPMRLAQLYGAAPSNLSIRLLD 478  
Qy 434 RKQEEARLTLAQL--GTQQAAREPPAGPPAFSLHSEVSVLKDQLQACRGFYQDGRGDR 491  
Db 479 QASHSAGTKAPALKGGAEIRPP-----DVGHVRLMLGKMCAPRYPSGGAWDPH 528  
Qy 492 RAEGPAKRPFGQKWLIDLQKNS-----ENPMRDLFLMAVQLNRHEMATYFWAMGQ 542  
Db 529 -----PQGFGESEMYLLSDKATPSLSDAGLQAPWSDLLWALLNRAQWAMYFWEMGS 583  
Qy 543 EGVAAALAAACKILKENSHELEAFAARATREA--KYERLALDLFSECYSSEARAFALIV 600  
Db 584 NAVSSALGACLLURVWARLEPDAEAAARRKDLAFKFEKMGVDFLFGECYRSSEVRAARLL 643  
Qy 601 RNRKCSKTTCLHLATADAKAFFAHDGVOAFTRIWWGDMAGTPTLRLILGLFLCPALV 660  
Db 644 RRCLMGDAICLQALQADARAFQDGVOSLITQKWWGDMASTPTIHALVLAFFCPPLI 703  
Qy 661 YTNLITF--SEAPLRTGLLEDLODLSLDTKPSLYGLQSRVEELVEAPRAQGD----- 712  
Db 704 YTRLITFRKEEBEPTRELE--FDMDSVINGEPPVGTADPAEKTPLGVPRQSGRPGCGG 761  
Qy 713 --RGPRAVFLTTWRKFWGAPVTFLGNVVMYAFILFVLYLLVDFRPPQPSGPEVT 770  
Db 762 RCGRRRC--LRWFHFWGAPVTIPMGVNVSYLLFLLFSRVLVDFQAP--PGSLELL 816  
Qy 771 LYFWFVTLVLEERQGFDTEDT-----HLVKFTLVGNWNKNCMDVAIFLPI 819  
Db 817 LYFWATLLCEELRQGLSGGSLASGGPGPHASLSQRULRYLAOSWQCDLVALTCFL 876  
Qy 820 VGVTCMLPSAFAGRTVAMDPMFTLRLIHFAIHKQLGPKIIIVVERMMKDVFFFLFF 879  
Db 877 LGVGCRLTPGLYHLGRVLCIDPMFTVTRALLHFTVKNQLGPKIVIVSKMKDVFFFLFF 936  
Qy 880 LSWLVAYGVTTQALLPHDGRLEWIFRVRVLYPIQIFQIPDLDEIDARV---NCSTH 936  
Db 937 LGWLVAYGATVTEGLLRPRDSDFSLRRVFRVRYPIQIFQIPQEDMDVALMEHSCSSE 996  
Qy 937 PLLLEDSP-----SCPSLYANMLVILLVTLVTLVNLMLLIAMFSYTFQVVOGNADM 991  
Db 997 PGFWAHPGQAAGTCVSQYANMLVLLLVIFLLVANILLNLIAMFSYTFQVVOGNADM 1056  
Qy 992 FWKFORNYLVEHHPALAPFILLSHLSLTLRRVFKK-----BAEHKREHLERD 1042  
Db 1057 YWKAQRYLRIRFHSRPPALAPPFIVISHLRLRLQLCRPRSPQSPSSPALEHFRVLSKE 1116  
Qy 1043 LPDPLDQKVVTWETOKENFLSKWEKRRDSEGEVLKRTAHRVDFTAKYLGGLRQEKRI 1102  
Db 1117 -----AERKLLTWESVHKNFLARARDKRESERLKRTSQKVDLALKQLGHIREVEQRL 1172  
Qy 1103 KCLESQINCSVLVSSVADVLQAG-----GGP 1129  
Db 1173 KVLREVOQCSRVGLWVAELRSALLPPGGP 1204

RESULT 13  
AAE20283  
ID AAE20283 standard; protein; 1214 AA.  
XX  
AC AAE20283;

XX 18-JUN-2002 (first entry)  
DT Human Trp9 protein.  
XX  
DE  
XX  
KW Human; prostate carcinoma associated protein; Trp9; Trp10a; Trp10b;  
KW transient receptor potential; calcium channel protein; Trp8a; Trp8b;  
KW molecular marker; endometrial cancer; uterine carcinoma; melanoma; gene;  
KW tumour; chorion carcinoma; lung cancer; antisense therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200210382-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 18-JUL-2001; 2001WO-EP008309.  
XX  
PR 28-JUL-2000; 2000US-0221513P.  
XX  
PA (WISS/) WISSENBEACH U.  
XX  
PI Wissenbach U;  
XX  
DR WPI; 2002-269013/31.  
DR N-PSDB; AAD32372.  
XX  
PT Novel isolated nucleic acid encoding human prostate carcinoma associated  
PT protein such as transient receptor potential 8a, 8b, 10a, 10b proteins,  
PT useful as molecular markers for diagnosing prostate cancer.  
XX  
PS Claim 1; Fig 9A; 70pp; English.  
XX  
CC The invention relates to human prostate carcinoma associated proteins  
CC such as transient receptor potential (Trp)8a, Trp8b, Trp9, Trp10a and  
CC Trp10b and nucleic acid molecules encoding such polypeptides. Trp8, Trp9,  
CC Trp10 are novel calcium channel proteins. Sequences of the invention are  
CC useful as molecular markers for diagnosing prostate cancer. Sequences of  
CC the invention, their antibodies, inhibitors and antisense molecules are  
CC useful for preventing, treating or ameliorating a prostate tumour,  
CC endometrial cancer (uterine carcinoma), tumour, a chorion carcinoma,  
CC cancer of the lung or melanoma. Polynucleotides of the invention are used  
CC in antisense therapy. The present sequence is human Trp9 protein  
XX  
SQ Sequence 1214 AA;

Query Match 40.1%; Score 2444.5; DB 5; Length 1214;  
Best Local Similarity 45.5%; Pred. No. 2.3e-222;  
Matches 533; Conservative 177; Mismatches 351; Indels 111; Gaps 26;

Qy 26 GSVNFGSGGKKGKFRVPVSGVAPSVLFDLLIAEHLPAFLNVLVSGEQPFAMKSWLR 85  
Db 76 GELDTGTAGRKHNSFLRSLDRDTPAAVYSLVTRTWGFRAPNLVSVLGGSGPVLQTLQ 135  
Qy 86 DVLRLKGLVKAQSTGAWILTSALRYGLARHGOAVRDHSLASTSTKRVVAVGMASIGRV 145  
Db 136 DLLRLGLVRAAGSTGAWIVTGLHGTGIGHGVAVVRDQMASTG-GTKVVAVMGVAPWGV 194  
Qy 146 LHRRILEPAEQDFPVHY-----PEDDGSQGPCLSDNSLHSHFVLVPEPGPGKGLTEL 200  
Db 195 RNRDTLINPKGSFPARYRWGPPED--GVQFP--LDYNYSAFFLVDVDDTHCLGENRF 249  
Qy 201 RLRLKHHISEQAGYGGTGTSTHPIVLCILVNGDPNLTLSRISRAVQOAPWLILVSGGTA 260  
Db 250 RLRLSYISQKTVGGTG-IDIVLILLIDGDEKMLTRIENATQAOLPCLLVAGSGAA 308  
Qy 261 DVLAALVNQPHLLVP-----KVAEKQFKEKPKSFHFWEDIVRWTKLQNTISHQHLL 313  
Db 309 DCLAETLED--TLAPSGGARQGEARDIRFFPK-----GDLEVLQAQVERIMTRKELL 361  
Qy 314 TVYDFEGSGEELDTVLKALVKACKSHSQBPQDYLDELKLAAMDVRDIAKSEIFNGDV 373  
Db 362 TVYSSE-DGSEEFETIVLKVKAC--GSSEASAYLDELRLAVANVRVDIAQSELFRGDI 418

QY	374	EWKSCDLEVMVDALVSNKPEFVVDNGADVADELTYGELQELVRSVRKSLLEDLQ	433
Db	419	QMRSFHLEASIMDALLDPFVLLISHGUSLGHFLTPMRLAQLYSAAPNSIRNLDD	478
QY	434	RKQBEARLTLAGL--GTQOAREPPAGPAPFSLHESVRVKDFLOQACRGFYQDGRPGDRR	491
Db	479	QASHSAGTKAPALGGAAELRPP-----DVGHVRLMLGKMCAPRYPSGGAWDPH	528
QY	492	RAEKGPAKPTGQKWLIDLNKS-----ENPWRDLFLWAVLONRHEMATYFWAMQ	542
Db	529	-----PGQFGESVYLLSDKATSPSLDAGLQAPWSDLLLWALLNRAQMAFYWENG	583
QY	543	EGVAALAAACILKEMSHLETEAARATREA--KYERLALDLSFSECVSNSEARAFALL	600
Db	584	NAVSSALGACULLRVMARLEDEAEARRKDLAFKFGEGVLDLFGECVRSSEVRAARLL	643
QY	601	FRNRCSWXTTCILHATEADAKAFHAGVQAFLTRIWMGDMAAGTPIRLILGAFICPALV	660
Db	644	ERCPLMGDATCLOLAWQADARAFQAQGVQSILITQKMGDMASITPIWALVLAPCPPLI	703
QY	661	YTNLITF--SBEAPURTGLELDLQDLSLDTESPLYGLQSRVEELVEAPRAQD-----	712
Db	704	YTRLITFRKSEEPRELE--FDMDSVINGEGPVGTADPAEKTPLGVPRSGRPGCCGG	761
QY	713	--RGPRAVFLTRMRKFWGAPVTVFLGNVMVYFAFLFVTVLLVDFRPPPOGPGPEVT	770
Db	762	RCGGRRC---LRWFHFGVGPVTIFMGNVSVYLLFLLFSRVLVDFQAP--FGSLELL	816
QY	771	LYFWFTVLVLEIRQFTDEDT-----HLVKFTLYVGDNNKNCMDVAIFLFI	819
Db	817	LYFWAFTLLCEBLRQGLSGGSLASGGPGPGHSHLSQRLRLYLADSNQCCLVALTCFL	876
QY	820	VQVTCRMPLPSAEAGRTVLAMDFVFTLRLHIFAIHKOLGPKIIVVERMKDVEFELEFF	879
Db	877	LGWGCRLTPGLYHGLRTVLCIDFMVFTVRLHIFTNKGQPKIVIVSKMKDVFEELEFF	936
QY	880	LSVWLVAVGVTTOALLHPDHGRLEWIFRVLRYPLQIFGQIPDLDEIDEARV---NCSTH	936
Db	937	LGWLVAVGATEGLLRPDSDFPSSILARVFRPYLQIFGQIPQEDMDVALMEHNSCSSE	996
QY	937	PLLEDSP-----SCPSLYANWLVLVLLVTFLLVNLVNLMLLIAMFSYTFQVQGNADM	991
Db	997	PGFWAHPPCAQAGTCVSQYANWLVLVLLVIFLLVANILLVNLIIAMFSYTFQVQGNSDL	1056
QY	992	FWKFORNYLVEYHERPALAPPILLSHLSITLRRVFKK-----BAEHKREHLERD	1042
Db	1057	YKKAQRYRLIRFHSRPAAPPFIVISHRLRLRLQLCRRPRSPQSPSPALEHFRVYLSKE	1116
QY	1043	LPDPLDOKVVTWETVOKENFLSKMKERRRDSSEGLRKTAAHVRVDFIATKYLGLGLEQEKRI	1102
Db	1117	----AERKLLTWESVHKEFNLLARARDKRESDSERLKRISQKVDLALKQLGHIREYEQRL	1172
QY	1103	KCLESGINYSVLVSSVADVLAQG-----GGP	1129
Db	1173	KVLEREVQCCSRVLGWVAEALSALLPPGGP	1204
RESULT 14			
ID	AAB85974	standard; protein; 1129 AA.	
XX	AC	AAB85974;	
XX	AC	AAB85974;	
DT	30-NOV-2001	(first entry)	
XX	DE	Human TLCC polypeptide.	
XX	KW	TLCC; transient receptor potential; TRP; TRP-like calcium channel; human;	
KW	KW	hepatotropic; cardiatic; antiarteriosclerotic; antiinflammatory; virucide;	
KW	KW	cytostatic; analgesic; cerebroprotective; nootropic; neuroprotective;	
XX	XX	gene therapy.	

OS	Homo sapiens.
XX	Key
XX	Location/Qualifiers
XX	1084..1129
FT	/note= "the residues in this region are not indicated in
FT	the sequence present in the sequence listing, but
FT	indicated in the Figure"
XX	WO200162794-A2.
XX	30-AUG-2001.
XX	20-FEB-2001; 2001WO-US005529.
XX	22-FEB-2000; 2000US-00510706.
PR	31-MAY-2000; 2000US-00583373.
PR	08-AUG-2000; 2000US-00634669.
XX	(MILL-) MILLENNIUM PHARM INC.
XX	Glucksmann MA, Curtis RAJ, Lora JM;
PI	WPI; 2001-557700/62.
DR	N-PSDB; AAH76383, AAH76384.
XX	New isolated nucleic acid encoding a transient receptor potential-like
PT	calcium channel for identifying modulators that can be used to treat
PT	hepatic or cardiovascular disorders.
XX	Claim 14; Fig 1A-D; 16pp; English.
XX	The invention provides isolated nucleic acids encoding a human transient
CC	receptor potential (TRP) family member, called TRP-like calcium channel
CC	(TLCC) polypeptide. The TLCC polypeptide can be expressed by standard
CC	recombinant methodology. The TLCC polynucleotides and polypeptide are
CC	used to identify modulators that can be used to treat a hepatic or a
CC	cardiovascular disorder, such as liver fibrosis or atherosclerosis. Other
CC	disorders that can be treated are hepatitis, liver tumours, cirrhosis of
CC	the liver, hemochromatosis, liver parasite induced disorders, central
CC	nervous system disorders, pain disorders, or disorders of cellular
CC	growth, differentiation or migration. The TLCC polynucleotides,
CC	polypeptide, protein homologs and antibodies to the proteins can be used
CC	in predictive medicine (e.g. diagnostic assays, prognostic assays,
CC	monitoring clinical trials and pharmacogenetics). Anti-TLCC antibodies
CC	can isolate TLCC proteins, regulate the bioavailability of TLCC
CC	proteins, and modulate TLCC activity. The present sequence represents the
CC	human TLCC polypeptide
XX	Sequence 1129 AA;
XX	Query Match 39.6%; Score 2412.5; DB 4; Length 1129;
XX	Best Local Similarity 45.6%; Pred. No. 2.3e-219;
XX	Matches 528; Conservative 174; Mismatches 346; Indels 111; Gaps 26;
QY	39 KFRVPSPGAPSVLPDILLAEHLPAPNLVSLVSGEEQPFAMKSLRDLVRLKGLVKAQS 98
Db	4 QFLRLSDRTDPAAYSLVTRTWGFRAPNLVSVLGGSGGPFVLTQWLQDLRLRGLVRAQS 63
QY	99 TGAWILTSALRVGLARHVGQAVRDHSHLASTSTKRVVAVGMAISLGRVLRHRIIEAQBDF 158
Db	64 TGAWITVGLTGTGHRHVGAVRDHQMSTG-GTKVAVMGAPVGVVNRDRLINPKGSF 122
QY	159 PVHY-----PEDDGGSGQLCSLDNSLHFLVPEPGPKGDLTELRLEKHISEQRA 213
Db	123 PARYVRWGDPE--GVQFF--LDVNYSAFLVDDGTGCLGENRFLRLRESYISQCKT 177
QY	214 GYGGTGISIEPVLCLLVNGDPTLBRISAVEQAAPMLIIVSGSGIADVLAAVLNQPILL 273
Db	178 GWGGTG-IDIPVILLIDGDKMLTRIENATQALPCLLVAGSGGADCLAEFLD--TL 234
QY	274 VP-----KVAEQPKFKSPKHSWEDIVRWTKLLQNTSHQLLITVYDFEQSGSEEL 326
Db	235 AFGSGGARQGEARDIRREFPK-----GDLEVLQAQVERIMTRKELLTVYSSE-DGSEEF 288

QY 327 DTVLKALVRACKSHSQEPQDYLDELKLAIVAMDRVDIAKGEIFENGDEWVKSCDLEEVMDV 386  
Db 289 ETIVLKVAC--GSSEASAYLDELAVANNEVDIAQELPRGDIQWSEFLEASLMD 346  
QY 387 ALVSNKPEFVRLFDVNGADVADFTYGRLOELVRSRKSLLFDLLQKQEEARLTLAGL 446  
Db 347 ALLNDREPEFVRLIISHGLSGHETPMRLAQLYSAAPSNLIRLLDQASHAGTKAPAL 406  
QY 447 --GTQOAREPPAGPPAFSLUEHSRVKDLFDQACRGFYQDGRCDRRAEKGAKRTGQ 504  
Db 407 KGAAELRPP-----DVGHVRLMLLKGMCAPRYPSGGAWDPH-----PGQGFGE 451  
QY 505 KWLLDLNQKS-----ENPWRDLFLWVLQNRHEMATYFWAMQGEVAAALAAACKIL 555  
Db 452 MYLLSDKATSPSLDAGLQAPWSLWALLNRAQWYFWMGNSNAVSSALGACILL 511  
QY 556 KEMSHLETEAEARATREA--KYERLALDLPSCYNSSEARAFALLVRRNRWKTCLH 613  
Db 512 RVNARLEPDAAEAARRKDLAFEGMGVDLFGECYRSSEVRAARLLLRCPWGDATCLQ 571  
QY 614 LATEADAKAPFAHDGVQAFUETRIWGDMAAGTPIRLLLGAFGLCPALVYTNLTF--SEEA 671  
Db 572 LAMQADARAFFAQDGVQSLTQKWDMASTTPIWALVLAFFCPPLIYTLITFRSSEE 631  
QY 672 PLRTGLDQLDLSLPTKSPXGLOSVEELVEAPRAQGD-----RGPRAVFLTR 723  
Db 632 PTREELE--FDMDSVINGEGEVCTADPAEKTPLGVPRQSGCGCGGRAC---LRR 686  
QY 724 WRKFGAPVTYVFGNVMYFAFLFTYVLLVDFRPPQPSGPEVTLVFWVFTVLEEI 783  
Db 687 WEFHFGAPVTIFMGNVVSYLLFLLSFVLLVDFQAP--PGSLELLLYFWAFTLCEEL 744  
QY 784 ROGEFTDEDT-----HLVKEFTLVGDNWKNKDMVAIFLTVGVTCHMLSAFE 832  
Db 745 RQLSGGSGSLAGGPGCHASUSQRLYLADSNQCDLVALTCPLLVGVCRLTTPGLXH 804  
QY 833 AGRTVLAMDVMFTLRLIHFALHKLQPKIIIVVERMKDKVFFFLFSLVWLVAYGVTTQ 892  
Db 805 LGRTVLICIDFMFTVRLHIFTVKNQKQPKIVISKMKDKVFFFLFSLVWLVAYGVAT 864  
QY 893 ALLHPHGDLEWIFRVLRYRPIYQIFGQIDLEIDARV---NCSTHPLLEDSP----- 944  
Db 865 GLLRPRDSDFPSILRRVFRVRYLQIFGQIDLEIDARV---NCSTHPLLEDSP----- 924  
QY 945 SCPSLYANWLVILLVTLVTLNVLNLLIAMFSYTFVQVGNADMFWMKFORYNLIVEY 1004  
Db 925 TVQSVQANWLVLLVIFLLVANILLVNLNLIAMFSYTFKQVQNSDLVWKAQRYLIREF 984  
QY 1005 HERPALAPPFILLSHLSLTLRRVFXK-----BAEHKREHLERDLPDLDQKVVTWE 1055  
Db 985 HSRPALAPPFIVISHLRLRLQCRPRSPQSPSPALEHFRVYLSKE----AERKLLTWE 1040  
QY 1056 TVOKENFLSKMEKRDRDSEGEVLKTAHRVDIAKYGLGRQEKIKLESQINVCVSL 1115  
Db 1041 SVHKNFLNARADREDSERLKRSTQKVDLALKOLGHIREVEQRLKVLEREVOQCSRV 1100  
QY 1116 VSSVADVLAQ-----GGP 1129  
Db 1101 LGWVAELSRALLPPGGP 1119  
RESULT 15  
ABG72088  
ID ABG72088 standard; protein; 1083 AA.  
AC ABG72088;  
XX  
XX 11-FEB-2003 (first entry)  
XX Human transient receptor potential (TRP)-like calcium channel (TLCC).  
XX Human; transient receptor potential-like calcium channel; TRP; TLCC;

18607; calcium signalling; growth; differentiation;  
capacitative calcium channel; store-operated calcium channel; SOC;  
plasma membrane; calcium ion; cytosol; modulator; membrane excitability;  
action potential; excitation; neurite outgrowth; synaptogenesis;  
signal transduction; angiogenesis; cell proliferation; vascular  
gene therapy; diagnosis; cardiovascular disorder; atherosclerosis;  
restenosis; endothelial cell disorder; tumour metastasis; psoriasis;  
rheumatoid arthritis; diabetes; hepatic disorder; hepatitis; cirrhosis;  
central nervous system disorder; Alzheimer's disease;  
Parkinson's disease; multiple sclerosis; epilepsy; cancer;  
cellular proliferation disorder; migration disorder; therapeutic.  
Homo sapiens.

Key Location/Qualifiers  
Region 1. .1083  
/note= "This region is shown as SEQ ID NO:2 in the  
sequence listing of the specification, but is only a  
shorter version of SEQ ID NO:2 shown in Figure 1"

US2002142377-A1.  
03-OCT-2002.  
20-FEB-2001; 2001US-00789481.  
22-FEB-2000; 2000US-00510706.  
31-MAY-2000; 2000US-00583373.  
08-AUG-2000; 2000US-00634669.

(GLUC/) GLUCKSMANN M A.  
(CURT) CURTIS R A J.  
(LORA/) LORA J M.

Glucksmann MA, Curtis RAJ, Lora JM;  
WPI: 2003-102516/09.  
N-PSDB; ABS58041.

Isolated transient receptor potential-like calcium channel polypeptide,  
useful for treating cardiovascular, hepatic, central nervous system  
disorders, pain, cellular proliferation, or migration disorder.

Claim 14; Fig 1; 80pp; English.

The invention discloses an isolated transient receptor potential (TRP)-  
like calcium channel (TLCC) polypeptide (18607). Calcium signalling has  
been implicated in the regulation of a variety of cellular responses,  
such as growth and differentiation. TLCC is a member of the capacitative  
calcium channel group or store-operated calcium channel (SOC) which is  
activated in the plasma membrane to import calcium ions from the  
extracellular environment to the cytosol. The nucleic acids, polypeptides  
and antibodies of TLCC are useful for detecting its presence in a sample,  
for identifying a compound which binds to it and identifying a compound  
which modulates its activity. Modulators of TLCC can be used to modulate  
membrane excitability, wave forms and frequencies of action potentials,  
thresholds of excitation, neurite outgrowth and synaptogenesis, signal  
transduction, angiogenesis, endothelial cell proliferation and vascular  
tone. The nucleic acid and polypeptide are also useful (using gene  
therapy) for diagnosing and treating cardiovascular disorders, such as  
atherosclerosis and restenosis, endothelial cell disorders, such as  
tumour metastasis, psoriasis, rheumatoid arthritis and diabetes, hepatic  
disorders such as hepatitis and cirrhosis, central nervous system disorders,  
such as Alzheimer's disease, Parkinson's disease, multiple sclerosis and  
epilepsy, cellular proliferation disorders, such as cancer, and growth,  
differentiation or migration disorders. TLCC can also be used in  
predictive medicine (e.g. diagnostic assays, prognostic assays,  
monitoring clinical trials and pharmacogenomics) and in methods of  
treatment (e.g. therapeutic and prophylactic). The sequence presented is  
the human TLCC, 18607, protein  
Sequence 1083 AA;

Query Match		38.6%;	Score 2353;	DB 6;	Length 1083;
Best Local Similarity		45.9%;	Pred. No. 9.9e-214;		
Matches 515;		Conservative 165;	Mismatches 336;	Indels 106;	Gaps 25;
Qy	39	KFVRVPGVAPSVLFDLLAEWHLPAPNLVSVLVBEBEOPFAMKSNLDRDLVRKGLVKAQAS	98		
Db	4	QFLRLSRTDPAAYSLVTRTWGFRAPNVLVSVLGGSGPVLTWLQDLRLRGLVRAQS	63		
Qy	99	TGAMILTSARVLARHVGQAVRDSLASTSTKVRVAVGMAISLGRVLHRLIEAEQEDF	158		
Db	64	TGAMIVTGLHTGIRHVGAVRDOMASTG-GTKVAVMGVAPGVVNRDTLTPKGSF	122		
Qy	159	PVHY-----PEDDGSQPLCSLDSNLSHFILVBPPEKGDGLTELRLEKHISEQRA	213		
Db	123	PARYWRGDPED--GVQFP---LDYNSAFFLVDDGTHGLGGENRFLRLSYISQOKT	177		
Qy	214	GYGTGSTEIPVLCILVNGDPNTLERISRAVEQAAPWLLIVSGGDIADVLAALVNPHLL	273		
Db	178	GVGGTG-IDIPVLLIIDGDEKMLTRIENATQAQLPCLLVAGSGGAADCLAEITLED--TL	234		
Qy	274	VP-----KVAEKQFKEKFPKSHFWSWEDIVRWTKLQNTITSHOHLITVYDFEGBSBE	326		
Db	235	APGSGARQGEARDIRFFPK-----GDLEVLQAQVERIMTRKELLITVYSSE-DGSEEF	288		
Qy	327	DTVILKALVKACKSHSQBPQDYLDELKLAVANDRVDIKASEIFNGDVEWKSCLDEEVMD	386		
Db	289	ETIVLALVKAC--GSSEASAYLDELRLAVANRVDIQAQSELFRGDIQWRSFHLEASLMD	346		
Qy	387	ALVSNKPEFVRLFDVNGADVADFTYGRLOELYSRSKSLFDLLQKQBEARLTLAGL	446		
Db	347	ALLNDRPEFVRLISHGLSHGFLTPMELAQLYSAAPNSLIRNLLDOASHSAGTKAPAL	406		
Qy	447	--GTQARPEPPAGPAPFSLHVEVSRVLFQDQACRGFYQDGRPGDRRAEKGPAPKPTGQ	504		
Db	407	KGAELRPP-----DVGHVRLMLLKKKCAPRYPSGGAWDPH-----PGQFGES	451		
Qy	505	KWLLDLNOKS-----ENPWRDLFLWAVLQNRHEMATYFWAMGQEGVAAALACKIL	555		
Db	452	MYLLSDKATSPLSLDAGLGQAPWSDLLLWALLNRAQWAMYFWEMGNSVASSALGACLL	511		
Qy	556	KEMSHLEYEAERATREA--KYERLALDLFSECYSNSEARAFALLVRNRCSKTTGLH	613		
Db	512	RYMAELEPDAEPAARKDLAFKFGMGVDLFGECYRSEVRAARLLLRRCPLWGDATCLQ	571		
Qy	614	LATEADAKAFFAHGQVQAFTRIMWGDMAAGPPIILLCGAFPCALVYTNLTTF--SEEA	671		
Db	572	LAMQADARAFFAQDQVQSLLTQKWGDMASTTPIWALVLAFFCPLIYTRLTITFRKSEB	631		
Qy	672	PLRTGLEDLQDLSLTESKSPLYGLQSRVEELVEAPRAQGD-----RGPRAVFLLTR	723		
Db	632	PTREELE--FDMDSVINGEPVGTADPAEKTPLGVPRQSGRPGCCGCGRRRC---LRR	686		
Qy	724	WKKFWCAPVTVPFGNVVMYFAELFTYVLLVDERPPQPGSGPEVTLXFWVPTLVLEI	783		
Db	687	WTFHWGAPVTIPFGNVVSYLLFLLFSRVLVDFQAP--PGSLELLLYFWAFTLLCEEL	744		
Qy	784	ROGFFTEDEPT-----HLVKKFTLYVGDNNKCDMVAIFLFGVTCRMLFSAFE	832		
Db	745	ROGLSGGGSLASGGPGCHASLSQRLRLYLADSNQCDLVALTCFLLVGCRLTPEGLYH	804		
Qy	833	AGRTVLAMDPMVFTLRLIHIPAIHKQLGPKIIVVERMMKDVFFFLFSLVWLVAVGTTQ	892		
Db	805	LGRTVLCIDFMVFTVRLHIFTVNKQLGPKIIVSKMMKDVFFFLFGLVWLVAVGATE	864		
Qy	893	ALLHPHDGRLMEIFREVLVRPYLQIPGLDEIDEARV---NCSTHPLLEDSP-----	944		
Db	865	GLLRPRDSPPSLRVRFPYLIQIPQIPQEDMDVALMEHNSCSSEPGFWAHPGQAQAG	924		
Qy	945	SCPSLYANMLVILLVTLVNTVNLMLLIAMFSYTFVQVQGNADMFWKFORYNLIVEY	1004		
Db	925	TCVSYQYANMLVLLVLLVAVANILLVNLIIAMFSYTFGKVGQNSDLYWKAQRYRLIREF	984		
Qy	1005	HERPALAPPFILLSHLSLTLRRVPFK-----BAEHKREHLERDLPDPLDQKVVTWE	1055		

Search completed: September 14, 2004, 00:04:28  
Job time : 80 secs

Db	985	HSRPAAPPFIVISHLRLQLCRRPRSPQSPSPALEHFRVYLSKE-----AERKULTWE	1040
Qy	1056	TVQKENFLSKMEKRRRDSGEVLRKTAHRVDFAIAYLGLGLRE	1097
Db	1041	SVHKENFLLARARDKRESDSERLAKTSQKVDLALKQLGHIRE	1082



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 14, 2004, 00:06:14 ; Search time 160 Seconds  
(without alignments)  
2335.021 Million cell updates/sec

Title: US-10-026-188-8

Perfect score: 6093

Sequence:

1 MDVQGPFGSPGDAEDRRE.....HRGLDGMQPGAGQPPSDT 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6093	100.0	1165	13	US-10-026-188-8
2	6093	100.0	1165	16	US-10-026-188-8
3	6057.5	99.4	1164	9	US-09-834-792-5
4	5088.5	83.5	1158	13	US-09-834-792-2
5	5088.5	83.5	1158	13	US-10-026-188-5
6	5008.5	82.2	1165	13	US-10-026-188-2
7	2448.5	40.2	1166	15	US-10-295-027-558
8	2448.5	40.2	1166	15	US-10-295-027-916
9	2448.5	40.2	1214	14	US-10-142-649-2
10	2444.5	40.1	1214	14	US-10-343-114-10
11	2412.5	39.6	1129	15	US-10-391-399-2
12	2353	38.6	1083	9	US-09-789-481C-2
13	2184.5	35.9	1040	16	US-10-312-354-44
14	2039	33.5	1503	12	US-10-369-022-48
15	2039	33.5	1503	12	US-10-405-793-21

16	2039	33.5	1503	13	US-10-007-706-1	Sequence 1, Appli
17	2039	33.5	1503	14	US-10-153-244-104	Sequence 104, App
18	2039	33.5	1503	14	US-10-210-152-21	Sequence 21, Appli
19	2039	33.5	1503	16	US-10-467-163-3	Sequence 3, Appli
20	1619	26.6	678	12	US-10-343-114-8	Sequence 8, Appli
21	1582	26.0	1104	14	US-10-171-319-8	Sequence 8, Appli
22	1567.5	25.7	1104	15	US-10-352-724-1	Sequence 1, Appli
23	1566.5	25.7	1095	9	US-09-759-143-778	Sequence 778, App
24	1566.5	25.7	1095	9	US-09-780-669-778	Sequence 778, App
25	1566.5	25.7	1095	9	US-09-822-827-778	Sequence 778, App
26	1566.5	25.7	1095	9	US-09-895-793-778	Sequence 778, App
27	1566.5	25.7	1095	9	US-09-895-814-778	Sequence 778, App
28	1566.5	25.7	1095	13	US-10-012-896-778	Sequence 778, App
29	1566.5	25.7	1095	14	US-10-205-823-421	Sequence 421, App
30	1566.5	25.7	1095	14	US-10-144-678A-778	Sequence 778, App
31	1566.5	25.7	1095	14	US-10-294-025-778	Sequence 778, App
32	1563.5	25.7	1104	15	US-10-295-027-566	Sequence 566, App
33	1563.5	25.7	1104	16	US-10-408-765A-3018	Sequence 3018, Ap
34	1563.5	25.7	1268	14	US-10-171-319-11	Sequence 11, Appli
35	1558.5	25.6	1095	9	US-09-759-143-780	Sequence 780, App
36	1558.5	25.6	1095	9	US-09-780-669-780	Sequence 780, App
37	1558.5	25.6	1095	9	US-09-822-827-780	Sequence 780, App
38	1558.5	25.6	1095	9	US-09-895-793-780	Sequence 780, App
39	1558.5	25.6	1095	9	US-09-895-814-780	Sequence 780, App
40	1558.5	25.6	1095	13	US-10-012-896-780	Sequence 780, App
41	1558.5	25.6	1095	14	US-10-144-678A-780	Sequence 780, App
42	1558.5	25.6	1095	14	US-10-294-025-780	Sequence 780, App
43	1549.5	25.4	1054	12	US-10-343-114-4	Sequence 4, Appli
44	1545.5	25.4	1104	15	US-10-352-724-3	Sequence 3, Appli
45	1499	24.6	665	16	US-10-763-992-25	Sequence 25, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-026-188-8  
; Sequence 8, Application US/10026188  
; Publication No. US20020164645A1  
; GENERAL INFORMATION:  
; APPLICANT: Zuker, Charles S.  
; APPLICANT: Zhang, Yifeng  
; TITLE OF INVENTION: The Regents of the University of California  
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific  
; TITLE OF INVENTION: Ion Channel  
; FILE REFERENCE: 02307E-1149100S  
; CURRENT APPLICATION NUMBER: US/10/026,188  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/259,379  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 1165  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human ltrpc6  
; US-10-026-188-8

Query Match 100.0%; Score 6093; DB 13; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDVQGPFGSPGDAEDRRELHHRGEVNFSGSKKRGKRVFVPSGVAPSVLFDLLLAEW	60
Db	1	MDVQGPFGSPGDAEDRRELHHRGEVNFSGSKKRGKRVFVPSGVAPSVLFDLLLAEW	60
QY	61	HLPAFLVSVLVEEQPFAMKSWLRLVKGILVKAQSTGAWILTSALRVGLARHVQAV	120
Db	61	HLPAFLVSVLVEEQPFAMKSWLRLVKGILVKAQSTGAWILTSALRVGLARHVQAV	120
QY	121	RHSLASTSTKRVVAVGVASIGRLVHRRILEEAQEDFFVHPEDDGGSGQLCSLDSNL	180

Db 121 RDHSLASTSTKRVVAVGMSGLRVLHRRILIEEAQEDFPVHYPEDDGGSGQPLCSLDSNL 180  
QY 181 SHFVLVEPPGPKGGDTLRLRLKHLSEORAGVGGTGSTIEIPVLCVLVNGDNTLRI 240  
Db 181 SHFVLVEPPGPKGGDTLRLRLKHLSEORAGVGGTGSTIEIPVLCVLVNGDNTLRI 240  
QY 241 SRVVEQAAPWLLVSGGGIADVLAAALVNQPHLLVPKVAEKQFKFSPKHSWEDIVRWT 300  
Db 241 SRVVEQAAPWLLVSGGGIADVLAAALVNQPHLLVPKVAEKQFKFSPKHSWEDIVRWT 300  
QY 301 KLLQNTITSHOHLTVYDFEQSGSELDVTILKALVKACKSHSQBPQDYLDLKLAVADR 360  
Db 301 KLLQNTITSHOHLTVYDFEQSGSELDVTILKALVKACKSHSQBPQDYLDLKLAVADR 360  
QY 361 VDIKSETFNGDVWKSCDLSEVMVDALVSNKPEFVRLFDVNGADVADFLTYGRLOELR 420  
Db 361 VDIKSETFNGDVWKSCDLSEVMVDALVSNKPEFVRLFDVNGADVADFLTYGRLOELR 420  
QY 421 SVSRKSLFLDLLQKQBEARLTLAGLGTQQAEPAGPPAFSLHEVSRVLKDFLQDACRG 480  
Db 421 SVSRKSLFLDLLQKQBEARLTLAGLGTQQAEPAGPPAFSLHEVSRVLKDFLQDACRG 480  
QY 481 FYQDGRPDGRRRAEKGPAKRTGQKWLDDLNQSENPRDPLFLWAVLQNRHEMATYFWAM 540  
Db 481 FYQDGRPDGRRRAEKGPAKRTGQKWLDDLNQSENPRDPLFLWAVLQNRHEMATYFWAM 540  
QY 541 GQEGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECYSNSSEARAFALLV 600  
Db 541 GQEGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECYSNSSEARAFALLV 600  
QY 601 RNRRCWSKTTCLHLATEADAKAFFADHGVQAFLTRIWMGDMAAGTPFILLGAFPCPALV 660  
Db 601 RNRRCWSKTTCLHLATEADAKAFFADHGVQAFLTRIWMGDMAAGTPFILLGAFPCPALV 660  
QY 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVVELVAPRAQDGRGPRAVFL 720  
Db 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVVELVAPRAQDGRGPRAVFL 720  
QY 721 LTRWRKFGAPVTVFLGNVMVYFAFLFTVYVLLVDPRPPQPGSGPEVTLYFWVFTLVL 780  
Db 721 LTRWRKFGAPVTVFLGNVMVYFAFLFTVYVLLVDPRPPQPGSGPEVTLYFWVFTLVL 780  
QY 781 EBIROGFTDETHLVKXFTLYVGNWNKCDMVAIFLFTVGTCTRMPLSAFEAGRTVLAM 840  
Db 781 EBIROGFTDETHLVKXFTLYVGNWNKCDMVAIFLFTVGTCTRMPLSAFEAGRTVLAM 840  
QY 841 DPMVFTLRLIHFALHKGPKIIIVVERMKDVFPLFLPSVWLYAYGVTTQALLHPHDG 900  
Db 841 DPMVFTLRLIHFALHKGPKIIIVVERMKDVFPLFLPSVWLYAYGVTTQALLHPHDG 900  
QY 901 RLEWIFRRLVYRPYLIQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLIV 960  
Db 901 RLEWIFRRLVYRPYLIQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLIV 960  
QY 961 TELLVTNVLNLLIAMSFTYFQVQGNADMFVKFQRYNLIYVEYHERPALAPFPILLSHL 1020  
Db 961 TELLVTNVLNLLIAMSFTYFQVQGNADMFVKFQRYNLIYVEYHERPALAPFPILLSHL 1020  
QY 1021 SUTLRVPKKEAHEKREHLERLDPDLDQKVVYTWETVQENFLSKWEXRRRDEGEVLK 1080  
Db 1021 SUTLRVPKKEAHEKREHLERLDPDLDQKVVYTWETVQENFLSKWEXRRRDEGEVLK 1080  
QY 1081 TAHRVDFTAKYLGGLREOEKRIKCLSEQINQSVLVSSVADVLAQGGPRSSQHCQGSQ 1140  
Db 1081 TAHRVDFTAKYLGGLREOEKRIKCLSEQINQSVLVSSVADVLAQGGPRSSQHCQGSQ 1140  
QY 1141 LVAADHRGCLDGWEQAGQPPSDT 1165  
Db 1141 LVAADHRGCLDGWEQAGQPPSDT 1165

US-10-408-765A-1150  
; Sequence 1150, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Faly, Boon D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: 660088.465  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1150  
; LENGTH: 1165  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-1150

Query Match 100.0%; Score 6093; DB 16; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCDVQGPSPGDAEDRRLGLHRGEVNFSGSKGRKGFVRVPSGVAPSVLFDLLLAEM 60  
Db 1 MCDVQGPSPGDAEDRRLGLHRGEVNFSGSKGRKGFVRVPSGVAPSVLFDLLLAEM 60  
QY 61 HLPAPNLVSVLVEEQEPFAMKSWLRLDLKGLVKAQSTGAWILTSALRVGLARHVQAV 120  
Db 61 HLPAPNLVSVLVEEQEPFAMKSWLRLDLKGLVKAQSTGAWILTSALRVGLARHVQAV 120  
QY 121 RDHSLASTSTKRVVAVGMSGLRVLHRRILIEEAQEDFPVHYPEDDGGSGQPLCSLDSNL 180  
Db 121 RDHSLASTSTKRVVAVGMSGLRVLHRRILIEEAQEDFPVHYPEDDGGSGQPLCSLDSNL 180  
QY 181 SHFVLVEPPGPKGGDTLRLRLKHLSEORAGVGGTGSTIEIPVLCVLVNGDNTLRI 240  
Db 181 SHFVLVEPPGPKGGDTLRLRLKHLSEORAGVGGTGSTIEIPVLCVLVNGDNTLRI 240  
QY 241 SRVVEQAAPWLLVSGGGIADVLAAALVNQPHLLVPKVAEKQFKFSPKHSWEDIVRWT 300  
Db 241 SRVVEQAAPWLLVSGGGIADVLAAALVNQPHLLVPKVAEKQFKFSPKHSWEDIVRWT 300  
QY 301 KLLQNTITSHOHLTVYDFEQSGSELDVTILKALVKACKSHSQBPQDYLDLKLAVADR 360  
Db 301 KLLQNTITSHOHLTVYDFEQSGSELDVTILKALVKACKSHSQBPQDYLDLKLAVADR 360  
QY 361 VDIKSETFNGDVWKSCDLSEVMVDALVSNKPEFVRLFDVNGADVADFLTYGRLOELR 420  
Db 361 VDIKSETFNGDVWKSCDLSEVMVDALVSNKPEFVRLFDVNGADVADFLTYGRLOELR 420  
QY 421 SVSRKSLFLDLLQKQBEARLTLAGLGTQQAEPAGPPAFSLHEVSRVLKDFLQDACRG 480  
Db 421 SVSRKSLFLDLLQKQBEARLTLAGLGTQQAEPAGPPAFSLHEVSRVLKDFLQDACRG 480  
QY 481 FYQDGRPDGRRRAEKGPAKRTGQKWLDDLNQSENPRDPLFLWAVLQNRHEMATYFWAM 540  
Db 481 FYQDGRPDGRRRAEKGPAKRTGQKWLDDLNQSENPRDPLFLWAVLQNRHEMATYFWAM 540  
QY 541 GQEGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECYSNSSEARAFALLV 600  
Db 541 GQEGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECYSNSSEARAFALLV 600  
QY 601 RNRRCWSKTTCLHLATEADAKAFFADHGVQAFLTRIWMGDMAAGTPFILLGAFPCPALV 660  
Db 601 RNRRCWSKTTCLHLATEADAKAFFADHGVQAFLTRIWMGDMAAGTPFILLGAFPCPALV 660  
QY 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVVELVAPRAQDGRGPRAVFL 720

Db 661 YTNLTITFSEAPRTGLELDQLDLSLDTSEKSPLYGLQSRVEELVEAPRAQCDRGPRAVFL 720  
QY 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPDPQSGPEVNTLYFWVFTVL 780  
Db 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPDPQSGPEVNTLYFWVFTVL 780  
QY 781 EETROGFFTDDETHLVKFKFTLYVGDNNKCDMVAIFLFIIVGVTCTMLPSAFAEAGRTVLAM 840  
Db 781 EETROGFFTDDETHLVKFKFTLYVGDNNKCDMVAIFLFIIVGVTCTMLPSAFAEAGRTVLAM 840  
QY 841 DMVFTLRILHIHFAIHKQLGPKIIVVERMMKOVFFFLFELSVMLVAYGVTTOALLHPHDG 900  
Db 841 DMVFTLRILHIHFAIHKQLGPKIIVVERMMKOVFFFLFELSVMLVAYGVTTOALLHPHDG 900  
QY 901 RLEWIFRRVLYRYPYLOIFGOIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLV 960  
Db 901 RLEWIFRRVLYRYPYLOIFGOIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLV 960  
QY 961 TFLVTVNLLMNLIIAMFSYTFQVQGNADMFWMKFORYNLIIVEYHERPALAPFPILLSHL 1020  
Db 961 TFLVTVNLLMNLIIAMFSYTFQVQGNADMFWMKFORYNLIIVEYHERPALAPFPILLSHL 1020  
QY 1021 SLTLRVFKKEAHEKHREHLERDLPDLPDQKVVTWETVQENFLSKMKERRRDEGEVLRK 1080  
Db 1021 SLTLRVFKKEAHEKHREHLERDLPDLPDQKVVTWETVQENFLSKMKERRRDEGEVLRK 1080  
QY 1081 TAHRVDFIAKYLGLREQEKRICKLESQINYSVLSSVADVLAQGGPRSSQHCQEGSQ 1140  
Db 1081 TAHRVDFIAKYLGLREQEKRICKLESQINYSVLSSVADVLAQGGPRSSQHCQEGSQ 1140  
QY 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165  
Db 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165

## RESULT 3

US-09-834-792-5  
; Sequence 5, Application US/09834792  
; Patent No. US20020037515A1  
; GENERAL INFORMATION:  
; APPLICANT: Mount Sinai School of Medicine of NYU  
; TITLE OF INVENTION: TRP8, A TRANSCIENT RECEPTOR POTENTIAL  
; FILE REFERENCE: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL  
; CURRENT APPLICATION NUMBER: US/09/834,792  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/197,491  
; PRIOR FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1164  
; TYPE: PRT  
; ORGANISM: Human  
US-09-834-792-5

Query Match 99.4%; Score 6057.5; DB 9; Length 1164;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1161; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 MODVQGPSPGDAEDRRELGLHRGEVNFVGGGKRGKRVFVPSGVAPSVLFDLILAEW 60

Db 1 MODVQGPSPGDAEDRRELGLHRGEVNFVGGGKRGKRVFVPSGVAPSVLFDLILAEW 60

QY 61 HLPAPNLVSVLGEQPFAMKSWLRDVLKGLVKAQSTGAMILTSALRVGLARHVQAV 120

Db 61 HLPAPNLVSVLGEQPFAMKSWLRDVLKGLVKAQSTGAMILTSALRVGLARHVQAV 120

QY 121 RDHSLASTSTKRVVAVGMASLGRVILHREAEQEDFPVHPEDDGGSGQPLCSLDSNL 180

Db 121 RDHSLASTSTKRVVAVGMASLGRVILHREAEQEDFPVHPEDDGGSGQPLCSLDSNL 180

## RESULT 4

US-09-834-792-2  
; Sequence 2, Application US/09834792  
; Patent No. US20020037515A1

QY 181 SHFIVPEPPGKGDGLTELRLLEKHIHQEAGYGGTGTGSIETPVLCLVNGDENTLIERI 240  
Db 181 SHFIVPEPPGKGDGLTELRLLEKHIHQEAGYGGTGTGSIETPVLCLVNGDENTLIERI 240  
QY 241 SRAVEQAAPWLILVSGGGIADVLALVNPQPHLLVPKVAEKQPKKEKFPKSHFSEMEDIVRWT 300  
Db 241 SRAVEQAAPWLILVSGGGIADVLALVNPQPHLLVPKVAEKQPKKEKFPKSHFSEMEDIVRWT 300  
QY 301 KLLQNTITSHQILLTVYDFEQEGSEELDTVILKALVKACKSHSQEPQDYLDLKLAVAWDR 360  
Db 301 KLLQNTITSHQILLTVYDFEQEGSEELDTVILKALVKACKSHSQEPQDYLDLKLAVAWDR 360  
QY 361 VDIKSEIEFNGDVEMKSCDLEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYR 420  
Db 361 VDIKSEIEFNGDVEMKSCDLEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYR 420  
QY 421 SVSRKSLLDLQKQKEEARLTLAGLGTQOAREPPAGPPAFSLHEYSRVRLKDFLODACRG 480  
Db 421 SVSRKSLLDLQKQKEEARLTLAGLGTQOAREPPAGPPAFSLHEYSRVRLKDFLODACRG 480  
QY 481 FYODGPGDRRAEKGPAKPTGOKWLLDLNOKSENPNWDLFLWAVLQNRHEMATYFWAM 540  
Db 481 FYODGPGDRRAEKGPAKPTGOKWLLDLNOKSENPNWDLFLWAVLQNRHEMATYFWAM 540  
QY 541 GQGVAAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSARAFALLV 600  
Db 541 GQGVAAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSARAFALLV 600  
QY 601 RNRCSWKTTCIHLATEADAKAFFAHDGVQAFELTRIMWGDMAAGTPIRLLLGAFCLPALV 660  
Db 601 RNRCSWKTTCIHLATEADAKAFFAHDGV-AFLTRIMWGDMAAGTPIRLLLGAFCLPALV 660  
QY 661 YTNLTITFSEAPRTGLELDQLDLSLDTSEKSPLYGLQSRVEELVEAPRAQCDRGPRAVFL 720  
Db 661 YTNLTITFSEAPRTGLELDQLDLSLDTSEKSPLYGLQSRVEELVEAPRAQCDRGPRAVFL 720  
QY 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPDPQSGPEVNTLYFWVFTVL 780  
Db 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPDPQSGPEVNTLYFWVFTVL 780  
QY 781 EETROGFFTDDETHLVKFKFTLYVGDNNKCDMVAIFLFIIVGVTCTMLPSAFAEAGRTVLAM 840  
Db 781 EETROGFFTDDETHLVKFKFTLYVGDNNKCDMVAIFLFIIVGVTCTMLPSAFAEAGRTVLAM 840  
QY 841 DMVFTLRILHIHFAIHKQLGPKIIVVERMMKOVFFFLFELSVMLVAYGVTTOALLHPHDG 900  
Db 841 DMVFTLRILHIHFAIHKQLGPKIIVVERMMKOVFFFLFELSVMLVAYGVTTOALLHPHDG 900  
QY 901 RLEWIFRRVLYRYPYLOIFGOIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLV 960  
Db 901 RLEWIFRRVLYRYPYLOIFGOIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLV 960  
QY 961 TFLVTVNLLMNLIIAMFSYTFQVQGNADMFWMKFORYNLIIVEYHERPALAPFPILLSHL 1020  
Db 961 TFLVTVNLLMNLIIAMFSYTFQVQGNADMFWMKFORYNLIIVEYHERPALAPFPILLSHL 1020  
QY 1021 SLTLRVFKKEAHEKHREHLERDLPDLPDQKVVTWETVQENFLSKMKERRRDEGEVLRK 1080  
Db 1021 SLTLRVFKKEAHEKHREHLERDLPDLPDQKVVTWETVQENFLSKMKERRRDEGEVLRK 1080  
QY 1081 TAHRVDFIAKYLGLREQEKRICKLESQINYSVLSSVADVLAQGGPRSSQHCQEGSQ 1140  
Db 1081 TAHRVDFIAKYLGLREQEKRICKLESQINYSVLSSVADVLAQGGPRSSQHCQEGSQ 1140  
QY 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165  
Db 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165

GENERAL INFORMATION:  
; APPLICANT: Mount Sinai School of Medicine of NYU  
; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL  
; FILE REFERENCE: AP32911 070165.0589  
; CURRENT APPLICATION NUMBER: US/09/834,792  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/197,491  
; PRIOR FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1158  
; TYPE: PRT  
; ORGANISM: Murine TRP8  
US-09-834-792-2

Query Match 83.5%; Score 5088.5; DB 9; Length 1158;  
Best Local Similarity 84.1%; Pred. No. 0;  
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY 1 MQDVQPRPGSGDAEDRELGLHRGEVNFSGGKKGKFKVPSGVAPSVLFDLLAEW 60  
DB 1 MQTQSSCGSPDPTDGEWEPILCRGEINFGSGKKGKFKVPSGVAPSVLFDLLAEW 60

QY 61 HLPAPNLVSVLGEERPLAMKSWLDRVLKGLVKAQAQSTGAWILTSALRVGLARHVQAV 120  
DB 61 HLPAPNLVSVLGEERPLAMKSWLDRVLKGLVKAQAQSTGAWILTSALRVGLARHVQAV 120

QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHYPEDGSGQPLCLSDS 178  
DB 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHYPEDGSGQPLCLSDS 178

QY 179 NLSHFILVPEGPPGKG-DGLTELRLRLEKHSIQAGYGGTGSIEIPIVCLLVGNDPNTL 237  
DB 179 NLSHFILVPEGPPGKG-DGLTELRLRLEKHSIQAGYGGTGSIEIPIVCLLVGNDPNTL 237

QY 181 NLSHFILVESGALSGNDGLTELQLSLEKHSIQAGYGGTGSIEIPIVCLLVGNDPNTL 240  
DB 181 NLSHFILVESGALSGNDGLTELQLSLEKHSIQAGYGGTGSIEIPIVCLLVGNDPNTL 240

QY 238 ERISRAVQAAFWLILVSGGGIADVIAALVNPQLLVPKVAEKQKFKPPSKHFSWEDIV 297  
DB 241 ERISRAVQAAFWLILVSGGGIADVIAALVNPQLLVPKVAEKQKFKPPSKHFSWEDIV 297

QY 298 RWTLLQNTSHQHLITVDFEGBSELDVTILKALVKACKSHQSEQDYDELKLA 357  
DB 301 HWTLLQNTSHQHLITVDFEGBSELDVTILKALVKACKSHQSEQDYDELKLA 357

QY 358 WDRVDIAKSEIFNGDVENKSCDLEVMVDALVSNKPEFVFLVDNGADVADFLTYGRLOE 417  
DB 361 WDRVDIAKSEIFNGDVENKSCDLEVMVDALVSNKPEFVFLVDNGADVADFLTYGRLOE 417

QY 418 LYRSVRSKSLFLDLQRKEEARLTLAGLTQQAAREPPAGPPAFSLHEYSRVLKDFLODA 477  
DB 421 LYHSVSPKSLFLDLQRKEEARLTLAGLTQQAAREPPAGPPAFSLHEYSRVLKDFLODA 477

QY 478 CRGFTQDGRDRRAEKGPAKPTGQKWLIDNOKSENPRDLFLWVLQNRHETATYF 537  
DB 481 CRGFTQDGRDRRAEKGPAKPTGQKWLIDNOKSENPRDLFLWVLQNRHETATYF 537

QY 538 WAMGQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSEYNSSEARAPA 597  
DB 537 WAMGQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSEYNSSEARAPA 597

QY 598 LVRNRNCKSTKTLHLATEADAKFAHGDGVQAFTRIHWGDMAGTPIRLLAGFTCP 657  
DB 597 LVRNRNCKSTKTLHLATEADAKFAHGDGVQAFTRIHWGDMAGTPIRLLAGFTCP 657

QY 658 ALVYNTLITFSEAPLRTGLELDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQGGPEA 717  
DB 657 ALVYNTLITFSEAPLRTGLELDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQGGPEA 717

QY 718 VELLTRWRKFWCAPVTFLGNVMVFAFLFTYVLLVDFRPPPGSGPSEVTLFVFWFT 777  
DB 717 VELLTRWRKFWCAPVTFLGNVMVFAFLFTYVLLVDFRPPPGSGPSEVTLFVFWFT 777

QY 778 LVLEETIRQGFDTDBDTHLVKKFTLYVCDNWNKCDMVAIFLFIYGVTCMLPSAFEAGRTV 837  
DB 777 LVLEETIRQGFDTDBDTHLVKKFTLYVCDNWNKCDMVAIFLFIYGVTCMLPSAFEAGRTV 836

QY 838 LAMDEWVFTLRLIHFALHKGQKGLIIVRMKMDVFFFLFFLSVWLVAIVGVTTCALHHP 897  
DB 837 LAIDFWVFTLRLIHFALHKGQKGLIIVRMKMDVFFFLFFLSVWLVAIVGVTTCALHHP 896

QY 898 HDGRLEWIFRRVLYRYPYLIQIFGQIPLDIDEARVNCSTHPLLEDSPSCSLYANWLVIL 957  
DB 897 HDGRLEWIFRRVLYRYPYLIQIFGQIPLDIDEARVNCSTHPLLEDSPSCSLYANWLVIL 956

QY 958 LLVTFLLVTNVLMLNLLIAMFSYTFVQVGNADWFKFORNLIVYHERPALAPPFLL 1017  
DB 957 LLVTFLLVTNVLMLNLLIAMFSYTFVQVGNADWFKFORNLIVYHERPALAPPFLL 1016

QY 1018 SHLSLTLRVRFKBAEHRLEHRLDPLDQKVVTTWETVQENFLSKMERKRRDSEGEV 1077  
DB 1017 SHLSLTLRVRFKBAEHRLEHRLDPLDQKVVTTWETVQENFLSKMERKRRDSEGEV 1076

QY 1078 LRKTAHRVDFTAKYLGGLRQEKRIKCLSEQINYSVSVADVLAQGGGPRSSQHCGE 1137  
DB 1077 LRKTAHRVDFTAKYLGGLRQEKRIKCLSEQINYSVSVADVLAQGGGPRSSQHCGE 1136

QY 1138 GSQVLAADHRGGLDGEQPGAGQPPSDT 1165  
DB 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 5  
US-10-026-188-5  
; Sequence 5, Application US/10026188  
; Publication No. US20020164645A1  
; GENERAL INFORMATION:  
; APPLICANT: Zuker, Charles S.  
; APPLICANT: Zhang, Yifeng  
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific  
; FILE REFERENCE: 02307E-114910US  
; CURRENT APPLICATION NUMBER: US/10/026,188  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/259,379  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 1158  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: mouse ltrpc5 predicted amino acid sequence  
US-10-026-188-5

Query Match 83.5%; Score 5088.5; DB 13; Length 1158;  
Best Local Similarity 84.1%; Pred. No. 0;  
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY 1 MQDVQPRPGSGDAEDRELGLHRGEVNFSGGKKGKFKVPSGVAPSVLFDLLAEW 60  
DB 1 MQTQSSCGSPDPTDGEWEPILCRGEINFGSGKKGKFKVPSGVAPSVLFDLLAEW 60

QY 61 HLPAPNLVSVLGEERPLAMKSWLDRVLKGLVKAQAQSTGAWILTSALRVGLARHVQAV 120  
DB 61 HLPAPNLVSVLGEERPLAMKSWLDRVLKGLVKAQAQSTGAWILTSALRVGLARHVQAV 120

QY 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHYPEDGSGQPLCLSDS 178  
DB 121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIE--EAQEDFPVHYPEDGSGQPLCLSDS 178

QY 179 NLSHFILVPEGPPGKG-DGLTELRLRLEKHSIQAGYGGTGSIEIPIVCLLVGNDPNTL 237  
DB 179 NLSHFILVPEGPPGKG-DGLTELRLRLEKHSIQAGYGGTGSIEIPIVCLLVGNDPNTL 237

QY 181 NLSHFILVESGALSGNDGLTELQLSLEKHSIQAGYGGTGSIEIPIVCLLVGNDPNTL 240  
DB 181 NLSHFILVESGALSGNDGLTELQLSLEKHSIQAGYGGTGSIEIPIVCLLVGNDPNTL 240

QY 238 ERISRAVQAAFWLILVSGGGIADVIAALVNPQLLVPKVAEKQKFKPPSKHFSWEDIV 297  
DB 241 ERISRAVQAAFWLILVSGGGIADVIAALVNPQLLVPKVAEKQKFKPPSKHFSWEDIV 297

QY 298 RWTLLQNTSHQHLITVDFEGBSELDVTILKALVKACKSHQSEQDYDELKLA 357  
DB 301 HWTLLQNTSHQHLITVDFEGBSELDVTILKALVKACKSHQSEQDYDELKLA 357

QY 358 WDRVDIAKSEIFNGDVENKSCDLEVMVDALVSNKPEFVFLVDNGADVADFLTYGRLOE 417  
DB 361 WDRVDIAKSEIFNGDVENKSCDLEVMVDALVSNKPEFVFLVDNGADVADFLTYGRLOE 417

QY 418 LYRSVRSKSLFLDLQRKEEARLTLAGLTQQAAREPPAGPPAFSLHEYSRVLKDFLODA 477  
DB 421 LYHSVSPKSLFLDLQRKEEARLTLAGLTQQAAREPPAGPPAFSLHEYSRVLKDFLODA 477

QY 478 CRGFTQDGRDRRAEKGPAKPTGQKWLIDNOKSENPRDLFLWVLQNRHETATYF 537  
DB 481 CRGFTQDGRDRRAEKGPAKPTGQKWLIDNOKSENPRDLFLWVLQNRHETATYF 536

QY 538 WAMGQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSEYNSSEARAPA 597  
DB 537 WAMGQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSEYNSSEARAPA 596

QY 598 LVRNRNCKSTKTLHLATEADAKFAHGDGVQAFTRIHWGDMAGTPIRLLAGFTCP 657  
DB 597 LVRNRNCKSTKTLHLATEADAKFAHGDGVQAFTRIHWGDMAGTPIRLLAGFTCP 656

QY 658 ALVYNTLITFSEAPLRTGLELDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQGGPEA 717  
DB 657 ALVYNTLITFSEAPLRTGLELDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQGGPEA 716

QY 718 VELLTRWRKFWCAPVTFLGNVMVFAFLFTYVLLVDFRPPPGSGPSEVTLFVFWFT 777  
DB 717 VELLTRWRKFWCAPVTFLGNVMVFAFLFTYVLLVDFRPPPGSGPSEVTLFVFWFT 776

238 ERISRAVEQAAPMLILVGGGSIADVLAAALVNQPHLLVPKVAEQKFKFKFSPKHSWEDIV 297  
241 ERISRAVEQAAPMLILVGGGSIADVLAAALVNQPHLLVPKVAEQKFKFKFSPKHSWEDIV 300  
298 RWYKLLQNTSHOHLITVYDFEQSGSELDLTVILKALVKACKSHSQBPQDYLDELKAVA 357  
301 HWTLLQNTSHOHLITVYDFEQSGSELDLTVILKALVKACKSHSQBPQDYLDELKAVA 360  
358 WDRVDIAKSIIFNGDVEWKSCLDEEVMVDALVSNKPEFVFLVDNGADVADFLTYGRLOE 417  
361 WDRVDIAKSIIFNGDVEWKSCLDEEVMVDALVSNKPEFVFLVDNGADVADFLTYGRLOE 420  
418 LYRSVRSKSLFOLLQKQOEAEALTLTLAGLCTQQAEPFPPAGPPAFSLHEVSRLVKDFLODA 477  
421 LYHSVPSKSLFELLQKQOEAEALTLTLAGLCTQQAEPFPPAGPPAFSLHEVSRLVKDFLODA 480  
478 CRGFYQDGRGDRRAEAKKILKEMSHLETEAARATREAKYERLALDLFSECYSSEARAPA 537  
481 CRGFYQDGRGDRRAEAKKILKEMSHLETEAARATREAKYERLALDLFSECYSSEARAPA 536  
538 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSSEARAPA 597  
537 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSSEARAPA 596  
598 LLVRRNRKWSKTTCLHLATEADAKAFPAHDGVQAFTRIWWGDMAAGTPIRLILGAFCLCP 657  
597 LLVRRNRKWSKTTCLHLATEADAKAFPAHDGVQAFTRIWWGDMAAGTPIRLILGAFCLCP 656  
658 ALVYTNLITFSEAPRTGLEDLQDLSLDTSEKSPYGLQSRVEELVEAPRAQDGRGPA 717  
657 ALVYTNLITFSEAPRTGLEDLQDLSLDTSEKSPYGLQSRVEELVEAPRAQDGRGPA 716  
718 VFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPSGSEVTLYFWVFT 777  
717 VFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPSGSEVTLYFWVFT 776  
778 LVLEERQGFDTDEDTHLVKKFTLYVEDNWNKCDMAIFLIVGVTCRMLPSAFEAGRTV 837  
777 LVLEERQGFDTDEDTHLVKKFTLYVEDNWNKCDMAIFLIVGVTCRMLPSAFEAGRTV 836  
838 LAMDMVFTLRILHIFAIHQKQPKIIIVERRMKOVFFFLFSLVWLVAYGVTQALLHP 897  
837 LAMDMVFTLRILHIFAIHQKQPKIIIVERRMKOVFFFLFSLVWLVAYGVTQALLHP 896  
898 HGRLEWIFRRLVYRPLQIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANMLVIL 957  
897 HGRLEWIFRRLVYRPLQIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANMLVIL 956  
958 LLVTFLLVNTVLLMNLIIAMFSYTFQVQGNADMFVKFQRYNLIYVHERPALAPPFILL 1017  
957 LLVTFLLVNTVLLMNLIIAMFSYTFQVQGNADMFVKFQRYNLIYVHERPALAPPFILL 1016  
1018 SHLSLTLRSVVEKEAHEHLEERDLPDLDQKVVTWETVQENFLSKMKRRRDEGEV 1077  
1017 SHLSLTLRSVVEKEAHEHLEERDLPDLDQKVVTWETVQENFLSKMKRRRDEGEV 1076  
1078 LRKTAHRVDIAKYIGLGLRQEKRIKCLBSQINVCVSVLVSSVADVLAQGGPRSSOHCE 1137  
1077 LRKTAHRVDIAKYIGLGLRQEKRIKCLBSQINVCVSVLVSSVADVLAQGGPRSSOHCE 1136  
1138 GSQVAAADHRGGIDGWEQPCAGQPPSDT 1165  
1137 RSQVAAADHRGGIDGWEQPCAGQPPSDT 1158

## RESULT 6

US-10-026-188-2  
; Sequence 2, Application US/10026188  
; Publication No. US20020164645A1  
; GENERAL INFORMATION:  
; APPLICANT: Zaker, Charles S.  
; APPLICANT: Zhang, Yifeng

; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific  
; FILE REFERENCE: 02307E-114910US  
; CURRENT APPLICATION NUMBER: US/10/026,188  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/259,379  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
; FEATURE:  
; OTHER INFORMATION: rat L-TRP taste predicted protein  
US-10-026-188-2

Query Match 82.2%; Score 5008.5; DB 13; Length 1165;  
Best Local Similarity 82.8%; Pred. No. 0;  
Matches 965; Conservative 77; Mismatches 113; Indels 11; Gaps 3;  
QY 1 MDVQPRPGSPGADRRRELGLHRGEVNFVGGSGKKRGKRVFVPSGVAPSVLFDLLABW 60  
Db 9 MPMAQSCSPGSPDITGDGWEPLCKGEVNFVGGSGKKRKFKVPSNVAPSMLELLTTEW 68  
QY 61 HLPAPNLVSLVGEEOFPAMKSWLRDLVRKGLVKAQSTGAWILTSALRVGLARHVQAV 120  
Db 69 HLPAPNLVSLVGEEOFPAMKSWLRDLVRKGLVKAQSTGAWILTSALRVGLARHVQAV 128  
121 RHSLASTSTKVRVAVAGMASLGRVLRRLIEAQEDFPVHYPEDDGGSGPLCSDLSNL 180  
129 RHSLASTSTKVRVAVAGMASLGRVLRRLIEAQEDFPVHYPEDDGGSGPLCSDLSNL 188  
181 SHFILVEPPGKG-DGLTELRLEKHIHQAGYGGTGSIEIPVLCILVNGDPTLER 239  
189 SHFILVEPPGKG-DGLTELRLEKHIHQAGYGGTGSIEIPVLCILVNGDPTLER 248  
240 ISRAVEQAAPMLILVGGGSIADVLAAALVNQPHLLVPKVAEQKFKFKFSPKHSWEDIV 299  
249 MSRAVEQAAPMLILVGGGSIADVLAAALVNQPHLLVPKVAEQKFKFKFSPKHSWEDIV 308  
300 TKLLQNTSHOHLITVYDFEQSGSELDLTVILKALVKACKSHSQBPQDYLDELKAVA 359  
309 TELLQNTSHOHLITVYDFEQSGSELDLTVILKALVKACKSHSQBPQDYLDELKAVA 368  
360 RVDIAKSIIFNGDVEWKSCLDEEVMVDALVSNKPEFVFLVDNGADVADFLTYGRLOE 419  
369 RVDIAKSIIFNGDVEWKSCLDEEVMVDALVSNKPEFVFLVDNGADVADFLTYGRLOE 428  
420 RSVRSKSLFOLLQKQOEAEALTLTLAGLCTQQAEPFPPAGPPAFSLHEVSRLVKDFLODA 479  
429 RSVRSKSLFOLLQKQOEAEALTLTLAGLCTQQAEPFPPAGPPAFSLHEVSRLVKDFLODA 488  
480 GFYQDGRGDRRAEAKKILKEMSHLETEAARATREAKYERLALDLFSECYSSEARAF 539  
489 GFYQDGRGDRRAEAKKILKEMSHLETEAARATREAKYERLALDLFSECYSSEARAF 544  
540 MGQEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSSEARAF 599  
545 MGQEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSSEARAF 604  
600 VRNRCWSKTTCLHLATEADAKAFPAHDGVQAFTRIWWGDMAAGTPIRLILGAFCLCP 659  
605 VRNRCWSKTTCLHLATEADAKAFPAHDGVQAFTRIWWGDMAAGTPIRLILGAFCLCP 664  
660 VYTNLITFSEAPRTGLEDLQDLSLDTSEKSPYGLQSRVEELVEAPRAQDGRGPA 719  
665 VYTNLITFSEAPRTGLEDLQDLSLDTSEKSPYGLQSRVEELVEAPRAQDGRGPA 724  
720 LLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPSGSEVTLYFWVFT 779  
725 LLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPSGSEVTLYFWVFT 784

QY 780 LEEIRQGFTEDETHLVKFTLYVGDNNKCDMVAIFLVGVTCRMLPSAFEAGRTVLA 839  
D 785 LEEIRQGFTEDETHLVKFTLYVEDNNKCDMVAIFLVGVTCRMLPSAFEAGRTVLA 844  
QY 840 MDMVFVTLRLIHFIAHKQLGPKIIVVERMMKOVFFFLFSLVWLVAYGVTTQALLPHD 899  
D 845 IDFWVFTLRLIHFIAHKQLGPKIIVVERMMKOVFFFLFSLVWLVAYGVTTQALLPHD 904  
QY 900 GRLEWIFRVRVLYRQIFQIPLDEIDEARVNCSTHPLLEDSPCSLYANWLVILL 959  
D 905 GRLEWIFRVRVLYRQIFQIPLDEIDEARVNCSTHPLLEDSPCSLYANWLVILL 964  
QY 960 VTFLLVTVNLLNLLIAMSFTFOVQGNADMFWKFORYNLIVYHERPALAPFILLSH 1019  
D 965 VTFLLVTVNLLNLLIAMSFTFOVQGNADMFWKFORYNLIVYHERPALAPFILLSH 1024  
QY 1020 LSLTLRVFKKAEHREHLERDLPDLDQKVVTWETVQKNFSLKMKRRDRDSEGEVLR 1079  
D 1025 LSLVLKQVRKEAQAQHQHRLERDLPDVPDQKIITWETVQKNFSLTMEKRRDRDSEGEVLR 1084  
QY 1080 KTAHRVDFIAKVLGLREOEKRIKLESQINVCVSVLVSSVADVLAAQGGGPRSSQHCGBGS 1139  
D 1085 KTAHRVDFIAKVLGLREOEKRIKLESQINVCVSVLVSSVADVLAAQGGGPRSSQHCGBGS 1144  
QY 1140 QLVAAHRRGGGLDGEQPGAGOPPSDT 1165  
D 1145 QPASARDREYLE-----AGLPHSDT 1164

RESULT 7  
US-10-295-027-558  
; Sequence 558, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsberg, Wendy M.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Glynn, Richard  
; APPLICANT: Hevezi, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
; FILE REFERENCE: 018501-01250005  
; CURRENT APPLICATION NUMBER: US/10/295,027  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US 09/663,733  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: US 60/350,666  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/335,394  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/332,464  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/334,393  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/340,376  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/347,211  
; PRIOR FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US 60/347,349  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: US 60/355,250  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 60/356,714  
; PRIOR FILING DATE: 2002-02-13  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 558  
; LENGTH: 1166  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-10-295-027-558  
  
Query Match 40.2%; Score 2448.5; DB 15; Length 1166;  
Best Local Similarity 45.6%; Pred. No. 6.1e-217;  
Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;  
  
QY 26 GEVNFSGSKRGKRVFVPSGVAPSVLFDLLLAELHLPAPNLVSVLGEVEQPFAMKSWLR 85  
D 28 GELDTGAGRKSHNPLRLSDRTDPAAYSLVTRTWGFRAPNLVSVLGGSGPVLQWLO 87  
QY 86 DVLRKGLVKAQASTGAMILTSALRVGLARHVQAVRDHSLASTSTKRVVAVAGMASGRV 145  
D 88 DLLRRGLVRAAQTSGAMIVTGLHTGIGRHVGVAVRDHMASTG-GTKVAVAGVAPWGV 146  
QY 146 LHRILBEAQDPPVHY-----PEDDGSQGPLCSLSDNLSHFLVVERPPGPKDGLTEL 200  
D 147 RNRDTLNPKGSPFARYRWGRDPD--GVQFP--LDYNSAFVLVDGTHGCLGGENRF 201  
QY 201 RLRLKHISEORAGVGTGSTEIPVLCVNVNDPNTLERISRAVEQAAPWILVSGSGIA 260  
D 202 RLRLSYISQKTVGGTG-IDIPVLLLIIDGDEKMLTRIENATQALPCLLVAGSGAA 260  
QY 261 DVLAALVNQPHLLVP-----KVAEKQKFKPSKHSWEDIVRWTKLQNLQIHSQHL 313  
D 261 DCLAEITLED--TLAPGSGARQGEARDIRRRFPK-----GDLEVLQAQVERIMTRKELL 313  
QY 314 TVYDFEQGSEBELDTVILKALVKAACKSHSQSPQDYLDLKLAVANDRVDAKSEIFNGDV 373  
D 314 TVYSSE-DGSEEFETIVLKALVKAC--GSSEASAYLDELRLAVANRVDIAQSELFGRDI 370  
QY 374 EWKSCDLEVMVDALVSNKPFVRLVDNGADVADFLTYGRLOELYSVRSKSLFDLLQ 433  
D 371 QWRSFHLEASLMDALNDPRPFVRLLIHSHGLSHGLFTPMRLAQIYSAAPSNSLIRNLD 430  
QY 434 RKQEEARLTLAGL--GTQOAREPPAGPPAFSLHSEVSRVLKDFLODACHFTQDQGRDR 491  
D 431 QASHSAGTKAPALKGAAELRPP-----DVGHVRLMLLGMKCAPRYPSGAWDPH 480  
QY 492 RAEGKPAKPTGQKWLLDLNQK-----ENPWRDLFWAVLONHEMATYFWAMQ 542  
D 481 -----PGQFGESMYLLSDKATSPSLDAGLQAPWSLWALLNRAQMANIYEWMS 535  
QY 543 EGVAALAAACKILKEMSHLETAEEAARATREA--KYERLALDLFSECYSNSARAFALIV 600  
D 536 NAVSALGACLLLRVMALEPDAEAEARKOLAFKFGGVDFLFGECYRSSEVRAARULL 595  
QY 601 RNRCSKTTCILHLATEADAKAFFAHDGVQAFPLTRIMWGDMAAGTPIRLLLGAFCLPALV 660  
D 596 RRCPLWGDATCLQAMQADARAFQAQDGVQSLTKQWGDMASTTPIWALVAFPCPLI 655  
QY 661 YTNLITF--SEAPARTGLDLDLSDTEKSPYGLQSRVEELVEAPRAQD----- 712  
D 656 YTRLITFRKSEEPTEELE--FDWDSVINGEGPVGTADPAEKTPLGVPRQGRGCCGG 713  
QY 713 --RGPRAVFLLTRMKFWGAPVTFLGNVMVFAFLFVLLVDFRPPPGPSGPEVT 770  
D 714 RCGGRC---LRWEHFWGAPVTIFGNVVSLLFLLFSLRVLLVDFQFAP--PGSLELL 768  
QY 771 LYFWVFTLVLEIRQGFTEDETHLVKFTLYVGDNNKCDMVAIFLVGVTCRMLPSAFEAGRTVLA 839  
D 769 LYFWAFTLLCEBLRQGLSGGGSGGPGGHASLSQRRLYRLADSNWQCDLVALTCLF 828  
QY 820 VGVTCMLPSAFEAGRTVLAIDFMVFTLRLLIHFIAHKQLGPKIIVVERMMKOVFFFLF 879  
D 829 LGVGCRLTPEGLYHLGRVLCIDFMVFTLRLLIHFIAHKQLGPKIIVVERMMKOVFFFLF 888  
QY 880 LSVWLVAIVGVTTQALLPHDGRLEWIFRVRVLYRQIFQIPLDEIDEARVNCSTHPLLEDSP 936  
D 889 LGVWLVAIVGVATEGLLRPRDSDFPSILRRVFRVLYRQIFQIPLDEIDEARVNCSTHPLLEDSP 948





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661 YTNLITF--SEEAPLRTGLEDLQDLSLDEKTEKSPYGLQSRVEELVEAPRAQGD-----712
704 YTRLITPRKSEBPTREELE--FDMDSVINGEGFVGTADEPAKCTPLGVPPQSGRPGCCGG761
713 --RGPRAVFLLTWRKFWGAPVTVFVLLVLLVDFRPPQSGPSGPEVT770
762 RCGRRRC--LRRWFHFWGAPVTFMGNNVSVYLLFLLFRVLLVDFQAP--PGSLLELL816
771 LYFVWFTLVLEIRQGFTEDETT-----HLVKFTLYVGDNNKCDMVAIFLI819
817 LYFVAFILLCEELRQGLSGGSLASGGPGCHASISQRLRLYLADSNQCDLVALTCFL876
820 VGTTCRMLPSAFAEAGRTVLAWDFVFTLRILHPIHAIKQLGPKLIIVVERWKKVFFLFF879
877 LGVGCRLTPGLYHLGRTVLCIDFMVFTVRLHIFTVANKQLGPKLIIVSKMKDVFFLFF936
880 LSWWLVAIVTTOALHPHDGRLEWIRRVLYRYLQIFGOIPLDEIDEARV--NCSTH936
937 LGVWLVAIVGATEGLLRPRDSFISILRRVRYRYLQIFGOIPOEDMDVALMEHSCSE996
937 PLILEDSP-----SCPSLIYANWLIVLLVTFLLVTVNLLMLLIAMFSYTFVQVGNADM991
997 PGFWAHPGCAAGTCVQYANWLIVLLVIFLLVANILLVLLIAMFSYTFKVQNSDL1056
992 FWKQRYNLIVYHERPALAPPFILLSHLSLTLRRVFK-----EAEKREHLERD1042
1057 YWKAQRYRLIREPHSRPALAPPFIVISHRLRLQLCRPRSPQSPSSALHEFRVLSKE1116
1043 LPDPLDQKVTWETVQKENFELSKMEKRRDSEGEVLRKTAHRVDFIAKYLGLGRQEKRI1102
1117 ----ABRKLTLWESVHKENFELARARCKRESDELKETSQKVDLALAKQLGHIREYEQRL1172
1103 KLESQINCVSVSVSVADVLAQG-----GGP1129
1173 KVLREVOCCSRVLGWVAEALSRSALLPPGGP1204

RESULT 10
US-10-343-114-10
; Sequence 10, Application US/10343114
; Publication No. US20040072998A1
; GENERAL INFORMATION:
; APPLICANT: Missenbach, Ulrich
; TITLE OF INVENTION: Trp8, Trp9 and Trp10, Novel Markers for Cancer
; FILE REFERENCE: 012627-034
; CURRENT APPLICATION NUMBER: US/10/343,114
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/EP01/08309
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-114-10

Query Match 40.1%; Score 2444.5; DB 12; Length 1214;
Best Local Similarity 45.5%; Pred. No. 1.5e-216;
Matches 534; Conservative 177; Mismatches 351; Indels 111; Gaps 26;

QY 26 GEVNFSGGKRGKRVFVSGVAPSVLFDLLIAEWHLPAPNLVSVLGVGEOPFAMKSWLR 85
Db 76 GELDTGAGRKHNSFLRSLDRTPAAVYSLVTRTWGFRAPNLVSVLGGSGPVLTWLQ 135
QY 86 DVLKGLVKAAGSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGMASLGRV 145
Db 136 DLLRRGLVRAAQSTGAWIVTGLHTGIGHVGVAVRDHQAQSTG-GTKVAVGAPWGVV 194
QY 146 LHRRIEEAQDEFPVHY-----PEDGGSGPLCSLDSNLSHFILLVEPFGPKGGLTEL 200
Db 195 RNRDTLNPKGSPFARYWRGDPED--GVQFP---LDVNSAFPLVDGTHGCLGGENRF 249

US-10-142-649-2
; Sequence 2, Application US/10142649
; Publication No. US20030143557A1
; GENERAL INFORMATION:
; APPLICANT: Penner, Reinhold
; TITLE OF INVENTION: Methods of Screening for TRPM4b Modulators
; FILE REFERENCE: A-71325-2/RFT/NBC
; CURRENT APPLICATION NUMBER: US/10/142,649
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/351,938
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-142-649-2

Query Match 40.2%; Score 2448.5; DB 14; Length 1214;
Best Local Similarity 45.6%; Pred. No. 6.6e-217;
Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;

QY 26 GEVNFSGGKRGKRVFVSGVAPSVLFDLLIAEWHLPAPNLVSVLGVGEOPFAMKSWLR 85
Db 76 GELDTGAGRKHNSFLRSLDRTPAAVYSLVTRTWGFRAPNLVSVLGGSGPVLTWLQ 135
QY 86 DVLKGLVKAAGSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGMASLGRV 145
Db 136 DLLRRGLVRAAQSTGAWIVTGLHTGIGHVGVAVRDHQAQSTG-GTKVAVGAPWGVV 194
QY 146 LHRRIEEAQDEFPVHY-----PEDGGSGPLCSLDSNLSHFILLVEPFGPKGGLTEL 200
Db 195 RNRDTLNPKGSPFARYWRGDPED--GVQFP---LDVNSAFPLVDGTHGCLGGENRF 249
QY 201 RLRLEKHSEQAGVGGTSGIETPVLVLVNDGPNPTLIRISRAVEQAAPWMLVSGGTA 260
Db 250 RLRLESYSIQKTVGGTG-IDIPVLLIIDGDKMLTRIENATQALPCLLVAGSGGAA 308
QY 261 DVLAALVNPHLLVP-----KVAEKQKEKFPSPKHSWEDIVRWTKLLQNLITSHQLL 313
Db 309 DCLAETLED--TLAPGSGGARQGEARDRIIRFPFK-----GDLEVLQAQVERIMTRKELL 361
QY 314 TVYDFEQSGSEELDTVLKALVKACKSHSQEPQDYLDLKLAVAVDRVDIAKSEIFNGDV 373
Db 362 TVYSSE-DGSEEFETIVLKVAC--GSSEASAYLDELRLAVMRVVDIAQSELFRGDI 418
QY 374 EWKSCDLEWMDVALVSNKPEFVRLVFDVADVADFTYCRLOELYRSVSRKSLPDLQ 433
Db 419 QWRSFHLEASLMDALLNDREPEFVRLIISHLGSLGHFTPMRLAQLYSAAPSNSLRNLLD 478
QY 434 RKQEEARLTLAGI--GTQQAPEPPGAPFAPSLHEVSRVLKDFLODQACRFYQDGRGDR 491
Db 479 QASHSAGTKAPALKGGAELRPP-----DVGHVLRMLLGRKWCAPRYPGSGAWDPH 528
QY 492 RAEGGAKRPTGOKWLLDLNQS-----ENPWRDLFLWAVLQNRHEMATYFWAMGQ 542
Db 529 -----PQGGEGSEMYLLSDXATPSLSDAGLQAPWSDLLWALLNRAQWAMYFEMGS 593
QY 543 EGVAALAAACKILKEMSHLETAAPARATREA--KYERIALDLFSECYSNSEARAFALLV 600
Db 584 NAVSSALGACLLLRVMARLEPDABEAARRKDLAPKPEGMGVDLFGECYRSSEVRAARLL 643
QY 601 RNRKWSKTTCLHATADAKAFPAHGVQAFLTRIWWGDMAAGTPTILRLGLAFLCPALV 660
Db 644 RRCPLWGDATCLQAMQADARAFPAQDGVQSLTLQKWWGDMASTTPIWALVLAFFCPLI 703

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QY 201 RLRLKEHISEQAGYGGTGTGSIIEPVLCLVNGDNPNTLERISRAVEQAAPWLLVVGSGIA 260
D 250 RLRLSEYISQKTVGGTGTG-IDIPVLLLLIDGDEKMLTRIENATQAQPLCLLVAGSGAA 308
QY 261 DVLAAVNQPHLLVP-----KVAEQKQKFKPSKHSFMSWEDIVRWTKLLQNTSHOHL 313
D 309 DCLAEITLED--TLAPGSGGARQGEARDIRRFEPK-----GDLEVLQAQVERIMTRKELL 361
QY 314 TVYDFEQQSEEDLTIVLKALVKACKSHSQEPQDYLDLKLAVAWDRVDIAKSEIFNGDV 373
D 362 TVYSSE-DGSEETIVLKALVKAC--GSSEASAYLDLKLAVAWNRVDIAQSELFGDI 418
QY 374 EWKSCDLEEVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOBLYSVSRKSLFLFLQ 433
D 419 QWRSFHEASLMDALLNDREFVRLLSHLSLGHFLTPMLQAQLYSAAPSNSLIRNLLD 478
QY 434 RKQEEARLTLAGL--GTQQAQREPPAGPAPASLHVSRVLKDFLODQACRGYQDGRPD 491
D 479 QASHAGTKAPALKGGAELRPP-----DVGHVLRMLLGMKCAPRYPGSGAWDPH 528
QY 492 RAEGKPAKRPCTGOKWLLDLNOKS-----ENPWEDLFLWALQNEHEMATYFWAMQ 542
D 529 -----FGQFGESMYLLSDKATSLSLDAGLQAPWSDLLWALLNRAQMAWYFWMGS 583
QY 543 EGVAALACKILKEMSHLETEAARATREA--KYERLALDFSECYSNSEARAFALLV 600
D 584 NAVSSALGACLLLRVMARLEPDAEAAARRKDLAFKFGMGVDLFGECYSSEVRAARLL 643
QY 601 RNRCKSKTKCLHLATEADAKAFPAHDGVAFTRIWGDMAAGTPILRLGLAFPCALV 660
D 644 RCPLMGDATICQLAWQADARAFQAGVQSLTQKWWGDMASTTPIWALVLAFFCPPLI 703
QY 661 YTNLIITF--SEBAPLTGLLEDOLDLDEKSLPLXGLOSREELVEARAQD----- 712
D 704 YRLITFRKSEBEPTEELB--FDMDSVINGEGVGTADPAEKTPLGVPRQSRPCCGG 761
QY 713 --RGPRAVFLTRKFWGAPVTVFLGNVVMYPAFLFTYVLLVDFRPPQPGSPPEVT 770
D 762 RCGGRRC--LRRWFHFWGVPTIFMGNVSYLLFLLLSRVLLVDFQAP--PGSLELL 816
QY 771 LYFWMFTVLLEETROGFFTDET-----HLVKFTLYVGNWKNCKDMVALFLFI 819
D 817 LIFWAPTLLEBELRQSLGSGGSLASGPGPGHASLSQRLRLYLDASNQCCLVALTCEL 876
QY 820 VGTICMLPSAFEAGRTVLAMPFMVFTLRLIHFAHKGQPKIIVVERMKDKVDFEFLF 879
D 877 LGVGCRLTGLYHGLTVCIDFMVFTVRLHIFTVKNQKQKIVIVSKMKDKVDFEFLF 936
QY 880 LSVLVAVGVTTOALLPHDGRLEWIFRRLVRYPYLQIFQIPLDDEARV---NCSTH 936
D 937 LGVNLVAVGATEGLLRPRSDPPSTLRRVRYPYLQIFQIPLDMDVALMEHNSCSSE 996
QY 937 PLLLEDSP-----SCPSLYANWLVLLVYLLVTVNLLMLLIAMFSTPOVQGNADM 991
D 997 PGFWAHPQGAQAGTCVQGANWLVLLVIFLLVANILLVLLIAMFSTYTFKGQNSDL 1056
QY 992 FMKFORNLIVYHERPALAPPFILLSHLSLTLRVFKK-----BAEHKRELERD 1042
D 1057 YWKAQRYLIRFHSERPALAPPFIVISHLRLRLQRCRRPSPQSPSSPALEHFRVYLSKE 1116
QY 1043 LPDPLDKVVTWETVOKENFLSKMRKRRDSRGEVLRKTAHRVDFIAYLGLRQEKKRI 1102
D 1117 ----AERKLLTWESVHKNFLLARARDKRESDESLKRTSKQVDLALKQLGHIREYQEL 1172
QY 1103 KCLSEQINCVSVLSSVADVLAQG-----GGP 1129
D 1173 KVLREVOQCRRVLGWAELSRALLPPGGP 1204
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RESULT 11

US-10-391-399-2

; Sequence 2, Application US/10391399

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; Publication No. US20030219806A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Lora, Jose M.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: NOVEL 18607, 15603, 69318, 12303, 48000,
; TITLE OF INVENTION: 52320, 5433, 38554, 57301, 58324, 55063, 52991, 59914, 59921
; TITLE OF INVENTION: AND 33751 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0200NMIM
; CURRENT APPLICATION NUMBER: US/10/391,399
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/789,481
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 09/634,669
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 09/583,373
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: US 09/510,706
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 10/309,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/336,936
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 10/094,214
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US60/275,078
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-391-399-2

Query Match      39.6%; Score 2412.5; DB 15; Length 1129;
Best Local Similarity 45.6%; Pred. No. 1.3e-213;
Matches 528; Conservative 174; Mismatches 346; Indels 111; Gaps 26;
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QY 39 KFRVPSPGAPSVLFDLLAEHLPAPNLVSLVSGEEQPFAMKSLRDVLRKGLVKAQS 98
D 4 QFLRLSDRTDPAAYVSLVTRTWGFRAPNLVSLVSGSGGVPVLTQDLRLRRGLVRAQS 63
QY 99 TGAWILTSALRGLARHVQAVRDHSLASTSTKRVAVAGMASLGRVLRHRIIEBAQEDF 158
D 64 TGAWITVGLTIGIRHVGVAVRDHMASTG-GTKVAVAGVAPGVVNRDRLINPKGSF 122
QY 159 PVHY-----PEDDGSQGLCLSDNSLHSHFVLVEPPGKGDGLTELRLRLEKHISORA 213
D 123 FARYWRGDPE--GVQFP--LDYNSAFFLVDDTGCLGGENRFRRLRESYISQOKT 177
QY 214 GYGGTGSIPIVLCILVNGDNPNTLERISRAVEQAAPWLLVVGSGGIADVLAALVNQPHLL 273
D 178 GVGGTG-IDIPVLLLLIDGDEKMLTRIENATQAQPLCLLVAGSGAACLAEITLED--TL 234
QY 274 VP-----KVAEQKQKFKPSKHSFMSWEDIVRWTKLLQNTSHOHLTVYDFEQQSEBEL 326
D 235 APGSGGARQGEARDIRRFEPK-----GDLEVLQAQVERIMTRKELLTVYSSE-DGSEEF 288
QY 327 DTIVLKALVKACKSHSQEPQDYLDLKLAVAWDRVDIAKSEIFNGDVWKSCLDEEVMD 386
D 289 ETIVLKALVKAC--GSSEASAYLDLKLAVAWNRVDIAQSELFGDIQWRGFHLEASLMD 346
QY 387 ALVSNKPEFVRLFDVNGADVADFLTYGRLOBLYSVSRKSLFLFLQKQKEARLTLAGL 446
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Db 347 ALLNDREPEVRLIIISHGLSLHFTLPMRLAQIYSAAPNSLIIRNLLDQASHSAGTKAPAL 406  
QY 447 --GTQARBPAGPPAPFSLHEVSRVLDKFDQACRGFYQDGRPCDRRRAEKGAKRPTGQ 504  
Db 407 KGGAAELRPP-----DVGHVRLMLGKMCAPRYPSGGAWDPH-----PGQGFGE 451  
QY 505 KWLDDLNQKS-----ENPWRDLFLWVLQNRHEMATYFWANGQEGVAAALAAACKIL 555  
Db 452 MYLLSDKATPLSLDAGLQAPWSDDLWALLNNAQWAMYFWENGNAVSSALGACLL 511  
QY 556 KEMSHLETEAARATREA--KYERLALDLFSEYCSNSEARAFALLVRRNRCWSKTTCLH 613  
Db 512 RVMARLEPDABEAAARRKDLAFKFGMGVLDLFGECYRSSEVRAARLLRRCPLMGDATCLO 571  
QY 614 LATEADAKAFPAHGVQAFTRIWMGDMAAGTPIRLILGALFCALVYTNLTIP--SEEA 671  
Db 572 LAMQADARAFPAQDGVQSLITQKMGDMASTTPIWALVLAFFCPPLIYTRILITFRKSEE 631  
QY 672 PLRTGLELDLSDTEKSPLYGLQSRVEBELVEAPRAQGD-----RGPRAVFLTLR 723  
Db 632 PTREBLE--FDMDSVINGEGPVGTADPAEKTPLGVPRQSGRPGCGGRCGRRC--LRR 686  
QY 724 WRKFWGAPVTIPLGNVVMYFAFLFTYVLLVDRPPPPQSGGPEVTILYFWVFTLVLEEI 783  
Db 687 WFHFAGAPVTIEMGNVVSLLFLLFSRVLLVDFQAP--PGSLELLYFWAFTLLCEEL 744  
QY 784 ROGFTEDEDT-----HLVKFTLYVGDNNKCDMVAIFLPIVGVTCRMLPSAFE 832  
Db 745 ROGLSGGGSLASGGPGGHASLSORLRLYLADSNQCDLVALTCFLGVGCRLLTGLYH 804  
QY 833 AGRTVLAMDPMVFTLRLIHFALHKGQEKIIVVERMMKDVFFFLFSLVMLVAYGVTTQ 892  
Db 805 LGRTVLCDIDFVFTVRLLIHIFTVNLKQGLPKIVISKMKDVFFFLFSLVMLVAYGVATE 864  
QY 893 ALLHPHGDRLWIFRRVLYRPVLIQIPGQIPDLDEIDARV---NCSTHPLLEDSP----- 944  
Db 865 GILLRPRDSDFFSILRRVYRPVLIQIPGQIPQDMDVALMEHSNCSSEFGFWAHPGGAQ 924  
QY 945 SCPSLYANWLVLLVFTLVNLLMILLIAMFSYTFVQVGNADMFWMKFORYNLIVEY 1004  
Db 925 TCVSYANWLVLLVIFULVANILLVLLIAMFSYTFKVGQNSDLVYKAQRYLIREF 984  
QY 1005 HERPALAPPFILLSHLSLTLRVRFK-----EAEKREHLERDLPDLDQKVVTWE 1055  
Db 985 HSRPALAPPFIVISHLRLRLQLCRRPSPQSPSPALSHFRVYLSKE-----AERKLLTWE 1040  
QY 1056 TVOKENFLSKMKRRRDSGEVLRKTAHVDFIAKVIGLREQEKRIKLESQINVCVSL 1115  
Db 1041 SVHKENFLARARDKRESDSRLKRTSKQVLDLALQGLHIRBYEORLKVLEREVQOCSR 1100  
QY 1116 VSSVADVLAQ-----GGP 1129  
Db 1101 LGWVAELSRALLPPGGP 1119

RESULT 12  
US-09-789-481C-2  
; Sequence 2, Application US/09789481C  
; Patent No. US20020142377A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria Alexandra  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Lora, Jose M.  
; TITLE OF INVENTION: 18607, A No. US20020142377A1e1 Human Calcium Channel  
; FILE REFERENCE: MNI-097CP3  
; CURRENT APPLICATION NUMBER: US/09/789, 481C  
; CURRENT FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 09/510, 706  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 09/634, 669  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 09/583, 373  
; PRIOR FILING DATE: 2000-05-31

; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1083  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-789-481C-2

Query Match 38.6%; Score 2353; DB 9; Length 1083;  
Best Local Similarity 45.9%; Pred. No. 3,9e-208;  
Matches 515; Conservative 165; Mismatches 336; Indels 106; Gaps 25;

QY 39 KFWRVGSGVAPSVLFDLLAEWHLPAPNLVSLVGEQPPFAMKSMRLDVLKGLKVAQAS 98  
Db 4 QFLRLSDRTDPAAYSLVTRTWGRAPNLVSVLGGSGPVLIQTLWQDLRLGLVRAQAS 63  
QY 99 TGAWILTSALRGLARHVGOAVRDHSLASTSTKRVVAVGMAISGRVHLRRILBEAQBD 158  
Db 64 TGAWIVTGGHGTGIRHVGVAVRDHOMASIG-GRKVVAMGVAPWGVVNRDRLINPKGSF 122  
QY 159 PVHY-----PDDGSGSQPLCSLDSNLSHFTLVPDPGPGKDGUTELRLRLKHISEORA 213  
Db 123 PARYVRWGRDPED--GVQFP--LDYNSAFPLVDDGTHGCLGGENRFRRLRESYISQOKT 177  
QY 214 GYGGTGIEIPVLCVNGDENTLERISRAVEQAAPWLLVSGSGIADVLAAALVNOPHLL 273  
Db 178 GVGGTG-IDIPVLLLLIDGDEKMLTRIENATQAOLPCLLVAGSGGAADCLAETLED--TL 234  
QY 274 VP-----KVAEKQFKEKFPKSHFSWEDIVRWTKLLQNITSHOHLFTVYDFRQGSBEL 326  
Db 235 APGSGGARQGEARDIRRFEPK-----CDLEVLQAQVERIMTRKELLTVYSSE-DGSEEF 288  
QY 327 DTVLKALVKACKSHSQEPDYDELKLAVADWRVDIAKSEIFNGDVEWKSCDLIEVMVD 386  
Db 289 ETIVLKVAC--GSSEASAYLDELRLAVANRVDIAQSELFRGDIQWRSFHLEASLMD 346  
QY 387 ALVSNKEPFEFLFVNDGNADVDELTYGELQELYSVSRSKSLFLLDLQKQBEARLTLAGL 446  
Db 347 ALLNDRPFVRLIIISHGLSLHFTLPMRLAQIYSAAPNSLIIRNLLDQASHSAGTKAPAL 406  
QY 447 --GTQARBPAGPPAPFSLHEVSRVLDKFDQACRGFYQDGRPCDRRRAEKGAKRPTGQ 504  
Db 407 KGGAAELRPP-----DVGHVRLMLGKMCAPRYPSGGAWDPH-----PGQGFGE 451  
QY 505 KWLDDLNQKS-----ENPWRDLFLWVLQNRHEMATYFWANGQEGVAAALAAACKIL 555  
Db 452 MYLLSDKATPLSLDAGLQAPWSDDLWALLNNAQWAMYFWENGNAVSSALGACLL 511  
QY 556 KEMSHLETEAARATREA--KYERLALDLFSEYCSNSEARAFALLVRRNRCWSKTTCLH 613  
Db 512 RVMARLEPDABEAAARRKDLAFKFGMGVLDLFGECYRSSEVRAARLLRRCPLMGDATCLO 571  
QY 614 LATEADAKAFPAHGVQAFTRIWMGDMAAGTPIRLILGALFCALVYTNLTIP--SEEA 671  
Db 572 LAMQADARAFPAQDGVQSLITQKMGDMASTTPIWALVLAFFCPPLIYTRILITFRKSEE 631  
QY 672 PLRTGLELDLSDTEKSPLYGLQSRVEBELVEAPRAQGD-----RGPRAVFLTLR 723  
Db 632 PTREBLE--FDMDSVINGEGPVGTADPAEKTPLGVPRQSGRPGCGGRCGRRC--LRR 686  
QY 724 WRKFWGAPVTIPLGNVVMYFAFLFTYVLLVDRPPPPQSGGPEVTILYFWVFTLVLEEI 783  
Db 687 WFHFAGAPVTIEMGNVVSLLFLLFSRVLLVDFQAP--PGSLELLYFWAFTLLCEEL 744  
QY 784 ROGFTEDEDT-----HLVKFTLYVGDNNKCDMVAIFLPIVGVTCRMLPSAFE 832  
Db 745 ROGLSGGGSLASGGPGGHASLSORLRLYLADSNQCDLVALTCFLGVGCRLLTGLYH 804  
QY 833 AGRTVLAMDPMVFTLRLIHFALHKGQEKIIVVERMMKDVFFFLFSLVMLVAYGVTTQ 892  
Db 805 LGRTVLCDIDFVFTVRLLIHIFTVNLKQGLPKIVISKMKDVFFFLFSLVMLVAYGVATE 864  
QY 893 ALLHPHGDRLWIFRRVLYRPVLIQIPGQIPDLDEIDARV---NCSTHPLLEDSP----- 944

Db 865 GLLRPRSDPFSILRRVFRPYLQIFQIQEDMDVALMEHNSCSSEPGFWAHPGQAQ 924  
Qy 945 SCPSLYANWLVLLVFLVTLVNLNLIAMSYTFQVQGNADMFWKFORNLIVEY 1004  
Db 925 TCVSOYANWLVLLVFLVTLVNLNLIAMSYTFQVQGNADLYWKAQRYLIREF 984  
Qy 1005 HERPALAPFFILLSHLSLTLRRVFKK-----EAEKHEHLERDLPODQKVWTE 1055  
Db 985 HSRPALAPFFIVISHLRLLRLQRCRRPRSPQSPALEHFRVYLSKE-----AERKLITWE 1040  
Qy 1056 TVQKENFLSKWEKRRRSEVLRKTAHRVDPIAKYJGGURE 1097  
Db 1041 SVHKEFLARADKRESDSERLKRSTQKVDLALKQLGHIRE 1082

## RESULT 13

US-10-312-354-44  
; Sequence 44, Application US/10312354  
; Publication No. US20040101930A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.; JACKSON, Jennifer L.;  
; APPLICANT: TANG, Y. Tom; YUE, Henry;  
; APPLICANT: ELLIOTT, Vicki S.; TRIBBLE, Catherine M.;  
; APPLICANT: LEE, Ernestine A.; RAMKUMAR, Jayalaxmi;  
; APPLICANT: LAL, Preeti G.; XU, Yuming;  
; APPLICANT: WARREN, Bridget A.; HAPALIA, April J. A.;  
; APPLICANT: BAUGHN, Mariah R.; AZIMZAI, Yalda;  
; APPLICANT: BATRA, Sajeev; BURFORD, Neil;  
; APPLICANT: YAO, Monique G.; NGUYEN, Darniel B.;  
; APPLICANT: LU, Dying Anna M.; CHAWLA, Narinder K.;  
; APPLICANT: GANDHI, Ameena R.; AU-YOUNG, Janice;  
; APPLICANT: ARVIZU, Chandra S.  
; TITLE OF INVENTION: SECRETED PROTEINS  
; FILE REFERENCE: PI-0133 USN  
; CURRENT APPLICATION NUMBER: US/10/312,354  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: US 01/19862  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: US 60/212,890  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: US 60/213,466  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/214,601  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/222,372  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 60/231,435  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: US 60/232,889  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PERL Program  
; SEQ ID NO 44  
; LENGTH: 1040  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 7690129CD1  
US-10-312-354-44

Query Match 35.9%; Score 2184.5; DB 16; Length 1040;  
Best Local Similarity 45.3%; Pred. No. 1-6e-192;  
Matches 486; Conservative 156; Mismatches 320; Indels 111; Gaps 26;  
Qy 125 LASTSKVRVAVGASIGRVLHRRILEAQEDFPVHY-----PEDGSGQPLCSLDSN 179  
Db 1 MASTG-GTKVAVGAPWGVNRDRLINPKGSFPARYWRGDPED--GVQFP---LDYN 54  
Qy 180 LSHFILLVEGPGKGDGLTELRLKLEHSEBQAGYGGTGSIEIPVLCVLLVNGDPTLTER 239  
Db 55 YSAFFLVLDGTHGCLGGENRFLRLUESYISQKTVGGTG-IDIPVLLLLIDGDEKMLTR 113

Qy 240 ISRAVEQAAPWLLVGGGGIADVLIALVNPQHLLVP-----KVAEKQKFKKPPSKHFS 292  
Db 114 IENATQQLPCLLVGGGAADCLAEITLED--TLAPGSGGARQGEARDRIRRFPFK----- 167  
Qy 293 WEDIVRMTKLQNTITSHOHLITVYDFQEGSEELDTVILKALVKACKSHSQEPQDYLDEL 352  
Db 168 -GDLEVLQAOVERIMTKELLTVYSSE-DGSEBEPETIVILKALVKAC--GSEASAYLDEL 223  
Qy 353 KLAVAMRVDIKSEIPNGDVEMKSCDLEEVMDVALVSNKPEFVRLVFDNGADVADFLTY 412  
Db 224 RLAVAMNRVDIAQSELFRGDIQWRSPHLEASLDALLNDPRPEFVRLILSHGLSLGHFLTP 283  
Qy 413 GRLOELYSVSRSKSLFLDLQKQEEARLTLAGI--GTQOARPEPPAGPPAFSLHEVSRLV 470  
Db 284 MRLAQLYSAAPSLSLRNLLDQASHAGTAGTKAPALKGAELRPP-----DVGHVL 333  
Qy 471 KDFLQDACRGFYQDGRPRDRRAEKGFAKPTQCKWLLDLNOKS-----ENWRDL 521  
Db 334 RMLLGRKCAPRYSGGAWDPH-----PGQFGESMYLLSDKATSPSLDGLGQAPWSDL 388  
Qy 522 FLMAVLQNHEMATYFWMGQEGVAAALACKILKEMSHLETEAEARATREA--KYERL 579  
Db 389 LLWALLINRAQMANFYEMGSAVSSALGACLLLRVMARLEPDAEAAAREKDLAFEGM 448  
Qy 580 ALDLFSECYSNSERAFALLVRNRCSKTTCLHLATEADAKAFHAGVQAFTRIWMG 639  
Db 449 GVDLFGEYSEVRARALLRRCLPWGDTCLQLAMQADARAFFAQDQGVQSILTKWMG 508  
Qy 640 DMAAGTPIRLILGAFCLPALVYTNLITF--SEBAPRTGLDQLDLSLDTKESPLYGLQ 697  
Db 509 DMASTPIWALVLAFCPLIYTRITFRKSEEPREELE--FDMDSVINGGGPVGTAD 566  
Qy 698 SRVEELVEAPAGGD-----RGPRAVFLTRMRKFWGAPVTVFLGNVVMYFAELFLF 749  
Db 567 PAEKTPLGVRQSGRPGCCGGRRC--LRWPHFWGAPVTIEMGNVSVLLFLLLF 623  
Qy 750 TVVLLVDFRPPQPGSGPEVTLYFWVTLVLEIRQGFTEDETT-----HUVKK 798  
Db 624 SRVLLVDFQAP--PGSLELLYFWAFTLLCBLRQGLSGGGSLASGGPGGHASLSQR 681  
Qy 799 FTLYVGDNNKCDMVAIFLVGVTCRMLPSAFAAGRTVLAMDPMVFTLRLIHFALHKQ 858  
Db 682 LRLYLADSNQCDLVALTCLFLGVGCRITPGLYHLGRTVLCIDFMVFTVRLLIHIFTVVKQ 741  
Qy 859 LQPKIIVVERMKDVFFLFFSVMLVAYGVTTQALLHHPDGRLEWIFRRLVYRPLQIF 918  
Db 742 LQPKIIVSKMKDVFFLFFSVMLVAYGVATEGLLRPRDSDFPSILRRVFRPLQIF 801  
Qy 919 GOIPLDEIDEARV--NCSTHPLLLLEDSP-----SCPSLYANWLVLLVTLVTLVNL 970  
Db 802 GOIPOEDMDVALMEHNSCSSEPGFWAHPGQAQTCVSOYANWLVLLVTLVTLVNL 861  
Qy 971 MNLLIAMFSYTFQVQGNADMFWKFORNLIVEYHERPALAPFFILLSHLSLTLRRVFKK 1030  
Db 862 VNLLIAMFSYTFQVQGNADLYWKAQRYLIREFHSRPAALAPFFIVISHLRLQLCR 921  
Qy 1031 -----EAEKHEHLERDLPODQKVWTEVQKENFLSKWEKRRRSEGEVIRKT 1081  
Db 922 PRSQPSSPALEHFRVYLSKE-----AERKLITWESVHKEFNFLARADKRESDSERLKT 977  
Qy 1082 AHRVDFIAKYLGLCEQEKRIKLCESQINYSVSVSVADVLAQG-----GSP 1129  
Db 978 SOKVDLALKQLGHIREYQRLKVLREYVQCCSRVLGVWVAEALSRSALLPPGGP 1030

## RESULT 14

US-10-369-022-48  
; Sequence 48, Application US/10369022  
; Publication No. US20030203847A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Rosenfeld, Julie Beth

APPLICANT: Silos-Santiago, Inmaculada  
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,  
TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,  
TITLE OF INVENTION: 27410, 32260, 619, 15985, 69112, 2158, 224, 615, 44373,  
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR  
TITLE OF INVENTION: 13424 MOLECULES  
FILE REFERENCE: MPI02-027P1RNMOMIN  
CURRENT APPLICATION NUMBER: US/10/369,022  
CURRENT FILING DATE: 2003-02-19  
PRIOR APPLICATION NUMBER: US 60/360,495  
PRIOR FILING DATE: 2002-02-28  
PRIOR APPLICATION NUMBER: US 60/370,121  
PRIOR FILING DATE: 2002-04-04  
PRIOR APPLICATION NUMBER: US 60/373,010  
PRIOR FILING DATE: 2002-04-16  
PRIOR APPLICATION NUMBER: US 60/373,908  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: US 60/377,717  
PRIOR FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: US 60/379,949  
PRIOR FILING DATE: 2002-05-13  
PRIOR APPLICATION NUMBER: US 60/382,409  
PRIOR FILING DATE: 2002-05-21  
PRIOR APPLICATION NUMBER: US 60/385,280  
PRIOR FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US 60/386,879  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/387,536  
PRIOR FILING DATE: 2002-06-10  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 48  
LENGTH: 1503  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-369-022-48

Query Match 33.5%; Score 2039; DB 12; Length 1503;  
Best Local Similarity 38.8%; Pred. No. 9.6e-179;  
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;  
26 GEVNFGGGKRGKRVFVSGVAPSVLFDLLAELHLPAPNIVLSVLGEEQPFAMKSMRLR 85  
128 GDIIVTGLSQKVKYRVSDTPSSVIVHLMTHQWGLDVENLLISVTGAKNFNKKPRLK 187  
86 DVLRKGLVKAAGSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGMASLGRV 145  
188 SIFRRLGVKAQTTGAWIITGSGHTGVKMQVGEAVRDFSLSSYKEGELITITIGVATWGT 247  
146 LHRRLIEEAQEDFPVHYPPDDGSGQGLCSLNSHFLVPEPPGPKGDGLTELRRLRL 205  
248 HRRGLIHTGFPFAEYILDEG-QGNLTCLNSHSHFLIVDDGTHGQYGVPELPLRL 306  
206 KHISEQAGYGGTGTIEIPVCLLVNGDPNTLIERISRAVEQAAPWILVSGSGIADVLA 265  
307 KFISETKRGGV-AIKIPICVWLEGGPGTLHTIDNATNGTPCVVWEGSGRVADVIAQ 365  
266 LVNQP--HLVVKVAEQ--PKEPEPKHFSWEDIVRTKLLQNTISQHLITVYDFEQ 320  
366 VANLPVSDITISLIQOKLSVFFQEMFET--FTESRIVETWTKIQDVRRRQLITVREGK 423  
321 EGSEEDLTIVLKALVKACKSHSQEPQDYLD-ELKLAIVAMDRVDIAKSEIFNGVVEWKS 379  
424 DGQDDVDVAILQALLKASQSDHFGHENWHLQKLAIVAMNVDIARSEIFMDEWQKPSD 483  
380 LBEVMVDALVSNKPEFVRLVFDVNGADVADFLTYGRLOEYVRSVRSKSLFDLLQKQEEA 439  
484 LHPTTAALISNKKPEFVKLFLENGVQLKEFTVMDTLLYLYENLDPSCLFHSKLQK---- 538  
440 RLTLAIGLGTQAREPPAGP--PAFSLHVSRLVKDFLQDACRGFYQDGRGDRRR----- 492

Db 539 -----VLVEDPBPACAPAPRLQMHVAVQLRELLGDFLTQPLYPHNDRLRLLLPV 592  
Qy 493 -----AEKGPAPKPTQKWLDLNOKSENPRDLFLWAVLQNRHEWATVFWAMQ 542  
Db 593 PHVKLVQGVSLRSLYKSSGHVTF-----TMDPIRDLITAIWVQNRRELAIWQSQ 646  
Qy 543 EGVAAALAAACKILKEMSHLETEAAR---ATRAKVERLALDLFSCYCSNSEARAFALL 599  
Db 647 DCIAAALACSKILKELSEEDTDSSEMLALAE-EYEHRAIGVFTCYRDEERAKLL 705  
Qy 600 VRRNRCKSTTCLHLATEADAKAFPAHDGVQAFITRIWGDMAAGTPTLRLILGLAFLCPAL 659  
Db 706 TRVSEANGKTTCLQALAEAKDMKVSHGGIOAFITKWWGQLSVNDGLWRVTLCLMIAFPL 765  
Qy 660 VYTNLITFSEBAPLRTGLDQLDLSLDTESPLYGLQSRVEELVAPRAQDGRPAVF 719  
Db 766 LLTGLISFREKR-----LQD-----VGTAAA----- 786  
Qy 720 LLTRKRFWAGAPVTVFVGNVVMYFAFLFVTVLLVDFRPPPPQSGSEVTLYFWVFTLV 779  
Db 787 ---RARAFPTAPVVVPHNLISYFAFLCLFAVLMVDFQPV---PSWCECAIYIWLFLSLV 840  
Qy 780 LEBIRQGFPTDETHLVKVKFTLYVGDWNKCDMAIFLIVGVTCRMLPSPAFAEAGRTVLA 839  
Db 841 CEEMRQULFYDPDECGLMKKAALYFSDFWNKLDVGAILLVAGLTCLLIPATLYPGRVILS 900  
Qy 840 MDMVFTLRLIHFPAIHKQLGPKIIVVERMMKDVFFFLFSLVWLVAVGVITQALLHPHD 899  
Db 901 LDFILFCLRLMHIFTISKTLPKIIIVRRMMKDVFFFLFLLAVVWVSEGVAKQAILIHN 960  
Qy 900 GRLEWIFRVLRYRVLQIFGOIP--LDEIDEARVNC--THPLLEDSPSCPS----- 948  
Db 961 RVDMLFRGAVYHSYLTIFGQIPGVIGVNNPHECHSPNGTDPY----KPKCPESDATQQ 1016  
Qy 949 --LVANMLVILLVTFLLVTVNLLMLLIAMFSYTFVQVGNADMEKFPQRYNLIVEXHE 1006  
Db 1017 RPAPFEMITVLLCLYLFTNLLNLLLIAMENYTFQVQOEHTDQIKWFORHDLIEVHG 1076  
Qy 1007 RPALAPPFILLSLTLRVRVFKAEHREHLERDLPDLDQKVVTVETVOKENFLSKM 1066  
Db 1077 RPAAPPFILLSHLQLFKRVVLTAKRHKQKLNKNEEAALLSWEIYILKENYLNQR 1136  
Qy 1067 EKRERDSEGEVLRTAHRVDPIAKVL-----GGLREQEKRIKLESQINVCVSVSS 1118  
Db 1137 QFQQRQREPEKIEDISNKVDAMVDLLDPLKXSSM---EORLASLEEQAQTARALHW 1193  
Qy 1119 VADVLAAQGGPRSSQHCGEQSOLVAAD---HRGGLDGWEQPG 1157  
Db 1194 IVRTLRSQFSSEADVPITLASQKAAEEDPABFGGRKKTPEEP 1235  
RESULT 15  
US-10-405-793-21  
; Sequence 21, Application US/10405793  
; Publication No. US20030224450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER,  
; TITLE OF INVENTION: LTRPG3, AND SPLICE VARIANTS THEREOF  
; FILE REFERENCE: D0171A CIP  
; CURRENT APPLICATION NUMBER: US/10/405,793  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: US 60/309,544  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: US 10/102,152  
; PRIOR FILING DATE: 2002-08-01  
; NUMBER OF SEQ ID NOS: 322  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 21  
; LENGTH: 1503  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-405-793-21



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